

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
4 January 2001 (04.01.2001)

PCT

(10) International Publication Number
WO 01/00844 A2

- (51) International Patent Classification⁷: C12N 15/31, 15/55, 1/21, 9/18, C07K 14/34, C12P 13/08, C12Q 1/68 199 42 088.2 3 September 1999 (03.09.1999) DE
199 42 095.5 3 September 1999 (03.09.1999) DE
199 42 123.4 3 September 1999 (03.09.1999) DE
199 42 125.0 3 September 1999 (03.09.1999) DE
- (21) International Application Number: PCT/IB00/00943
- (22) International Filing Date: 23 June 2000 (23.06.2000) (71) Applicant: BASF AKTIENGESellschaft [DE/DE]; D-67056 Ludwigshafen (DE).
- (25) Filing Language: English
- (26) Publication Language: English
- (72) Inventors: POMPEJUS, Markus; Wenjenstrasse 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestrasse 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstrasse 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstrasse 42, D-67117 Limburgerhof (DE).
- (30) Priority Data:
- | | | |
|--------------|-------------------------------|----|
| 60/141,031 | 25 June 1999 (25.06.1999) | US |
| 199 31 562.0 | 8 July 1999 (08.07.1999) | DE |
| 199 31 634.1 | 8 July 1999 (08.07.1999) | DE |
| 199 31 412.8 | 8 July 1999 (08.07.1999) | DE |
| 199 31 413.6 | 8 July 1999 (08.07.1999) | DE |
| 199 31 419.5 | 8 July 1999 (08.07.1999) | DE |
| 199 31 420.9 | 8 July 1999 (08.07.1999) | DE |
| 199 31 424.1 | 8 July 1999 (08.07.1999) | DE |
| 199 31 428.4 | 8 July 1999 (08.07.1999) | DE |
| 199 31 431.4 | 8 July 1999 (08.07.1999) | DE |
| 199 31 433.0 | 8 July 1999 (08.07.1999) | DE |
| 199 31 434.9 | 8 July 1999 (08.07.1999) | DE |
| 199 31 510.8 | 8 July 1999 (08.07.1999) | DE |
| 60/143,208 | 9 July 1999 (09.07.1999) | US |
| 199 32 180.9 | 9 July 1999 (09.07.1999) | DE |
| 199 32 227.9 | 9 July 1999 (09.07.1999) | DE |
| 199 32 230.9 | 9 July 1999 (09.07.1999) | DE |
| 199 33 005.0 | 14 July 1999 (14.07.1999) | DE |
| 199 32 924.9 | 14 July 1999 (14.07.1999) | DE |
| 199 32 973.7 | 14 July 1999 (14.07.1999) | DE |
| 199 40 765.7 | 27 August 1999 (27.08.1999) | DE |
| 60/151,572 | 31 August 1999 (31.08.1999) | US |
| 199 42 076.9 | 3 September 1999 (03.09.1999) | DE |
| 199 42 079.3 | 3 September 1999 (03.09.1999) | DE |
| 199 42 086.6 | 3 September 1999 (03.09.1999) | DE |
| 199 42 087.4 | 3 September 1999 (03.09.1999) | DE |
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
— Without international search report and to be republished upon receipt of that report.
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/00844 A2

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION**

Related Applications

- 5 This application claims priority to prior U.S. Provisional Patent Application
Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial
No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No.
60/151572, filed August 31, 1999. This application also claims priority to prior German
Patent Application No. 19931412.8, filed July 8, 1999, German Patent Application No.
10 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July
8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent
Application No. 19931424.1, filed July 8, 1999, German Patent Application No.
19931428.4, filed July 8, 1999, German Patent Application No. 19931431.4, filed July
8, 1999, German Patent Application No. 19931433.0, filed July 8, 1999, German Patent
15 Application No. 19931434.9, filed July 8, 1999, German Patent Application No.
19931510.8, filed July 8, 1999, German Patent Application No. 19931562.0, filed July
8, 1999, German Patent Application No. 19931634.1, filed July 8, 1999, German Patent
Application No. 19932180.9, filed July 9, 1999, German Patent Application No.
19932227.9, filed July 9, 1999, German Patent Application No. 19932230.9, filed July
20 9, 1999, German Patent Application No. 19932924.9, filed July 14, 1999, German
Patent Application No. 19932973.7, filed July 14, 1999, German Patent Application No.
19933005.0, filed July 14, 1999, German Patent Application No. 19940765.7, filed
August 27, 1999, German Patent Application No. 19942076.9, filed September 3, 1999,
German Patent Application No. 19942079.3, filed September 3, 1999, German Patent
25 Application No. 19942086.6, filed September 3, 1999, German Patent Application No.
19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed
September 3, 1999, German Patent Application No. 19942095.5, filed September 3,
1999, German Patent Application No. 19942123.4, filed September 3, 1999, and
German Patent Application No. 19942125.0, filed September 3, 1999. The entire
30 contents of all of the aforementioned application are hereby expressly incorporated
herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals',
5 include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful
10 organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

15

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*
20 *glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in
25 industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SMP nucleic acids of the
30 invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

- 3 -

microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

- 5 -

due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize
5 sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the
10 generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of
15 such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-
20 encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
25 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
30 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ

- 6 -

ID NO:6, SEQ ID NO:8....). The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence
5 which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function
10 involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%,
15 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-
20 numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of
25 the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also
30 includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

- 7 -

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 5 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively 10 linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in 15 *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a 20 substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical 25 is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or 30 *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

- 10 -

agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (e.g., where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, e.g., pyruvate from modified *C. glutamicum*), or may have an indirect

- 11 -

impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (e.g., where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described e.g. in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (e.g., arachidonic acid), diols (e.g., propane diol, and butane diol), carbohydrates (e.g., hyaluronic acid and trehalose), aromatic compounds (e.g., aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

- 12 -

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

- 13 -

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

- 14 -

production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

5

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are
10 either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications
15 of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor"
20 includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty
25 acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley
30 & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), panthetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

- 16 -

The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
5 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
10 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

15 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
20 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA
25 synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical
30 indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

- 17 -

enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J. (1980) *Industrielle Mikrobiologie*, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. *Microbial Technology* 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

Kockova-Kratchvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Parnas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xylulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

5 The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for
10 glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy
15 that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anaerobes, have evolved such that they
20 possess both of these pathways.

The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by
25 the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate
30 cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO₂. The acetyl group of acetyl CoA then reacts with

- 21 -

the 4 carbon unit, oxaloacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO₂ molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle are transferred to NAD⁺ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*, coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

- 22 -

The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (*e.g.*, ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (*e.g.*, ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

- 23 -

the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

- 24 -

products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary
5 for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

10 In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum*
15 strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as
20 ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation
25 and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or
30 more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

- 25 -

reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

- 26 -

(*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (*e.g.*, SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the

- 27 -

genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

- 28 -

appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*,
5 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises
10 sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the
15 Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences
20 comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or
25 RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The
30 sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

- 29 -

RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and
5 amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as
10 "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence
15 for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

20 In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is
25 sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
30 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

- 30 -

87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited
5 ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*,
10 hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer
15 or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises
20 substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of
25 one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*
30 the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

- 31 -

nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
5 homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used
10 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the
15 protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine
20 chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
25 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention
30 are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

- 32 -

compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

- 33 -

a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to

5 calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the

10 lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%,

15 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (e.g., the *C.*

20 *glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the

25 SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on

30 their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

- 34 -

another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to
25 changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an
30 even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential
5 for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the
10 invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-
15 70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of
20 the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one
25 sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two
30 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that

5 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid

10 substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine,

15 threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same

20 side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

25 the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

30 are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

- 37 -

complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

- 38 -

galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

- 39 -

methyribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*, an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

25 B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

- 40 -

autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

5 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells.

25 Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, amy, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4,

30

- 41 -

usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors
5 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes
10 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic
15 Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis*
20 *thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

25 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors
30 typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

5 Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a
10 pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

15 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
20 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 *gnl0*-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 *gnl*). This viral polymerase is supplied by
25 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 *gnl* gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
30 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another
5 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

10 In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and
15 methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
20 New York (ISBN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989)
25 *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
30 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+,

- 44 -

pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). .

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.*

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

- 45 -

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

- 46 -

transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination
5 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.
10 For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
15 expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion,
20 truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has
30 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

5 Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes
10 preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein,
15 still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein
20 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by
25 dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from
30 the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum*.

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred

5 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as

10 oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a

15 nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least

20 about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity

25 values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described

30 herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

- 50 -

which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

- 5 In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in
- 10 another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or
- 15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of
- 20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

- Biologically active portions of an SMP protein include peptides comprising
- 25 amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein.
- 30 Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

5 SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard
10 protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

15 The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a
20 protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of
25 the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian
30 host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

- 52 -

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends, as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide).
15 An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the
20 activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway
25 which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid
30 level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

- 53 -

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a
5 degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3;
10 Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding
15 sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
20 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
25 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
30 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

- 54 -

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a
5 variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the
10 following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a
15 cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.
25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

- 5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
- 10 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

- The nucleic acid and protein molecules of the invention may also serve as
- 15 markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
- 20 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the
- 25 invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

- The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which
- 30 the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

- 56 -

evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

- 57 -

unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO₂ production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum*.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXS02735	VV0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
9	10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
37	38	RXN01365	VW0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
53	54	RXA0206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
63	64	RXN01225	VW0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4.2.1.11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VW0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PYRUVATE KINASE (EC 2.7.1.40)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXN00635	VW0135	22708	20972	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VW0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VW0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VW0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
105	106	RXN03083	VW0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	F RXA02326	VW0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE
115	116	RXN02327	VW0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE
119	120	RXN02328	VW0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VW0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	VV0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
137	138	RXN01952	VV0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	VV0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	VV0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	VV0127	3127	2240	IOLB PROTEIN
155	155	F RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE.
157	158	RXN02829	VV0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VV0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VV0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	VV0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	VV0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	VV0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	VV0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	VV0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VV0009	3477	2296	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VV0009	3703	3533	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Glycerol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	VV0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
197	198	RXN01891	VV0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VV0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC 1.1.1.1)
219	220	RXN03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VV0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VV0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VV0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00868	VV0127	2230	320	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
231	232	RXN01143	VV0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VV0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VV0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239	240	RXA02453	GR00710	6103	5351	ACETON(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VV0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycle

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	645	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

- 64 -

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXN00013	VV0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VV0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VV0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VV0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VV0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VV0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXN02654	VV0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VV0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VV0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VV0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VV0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VV0006	6616	7050	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
353	354	RXN01369	VW0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VW0184	1	1890	GLYCOTEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
365	366	F RXA01884	GR00539	3	1475	GLYCOTEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
367	368	RXA01111	GR00306	16981	17427	GLYCOTEN OPERON PROTEIN GLGX (EC 3.2.1.-)
369	370	RXN01550	VW0143	14749	16260	GLYCOTEN PHOSPHORYLASE (EC 2.4.1.1)
371	372	F RXA01550	GR00431	3	1346	GLYCOTEN PHOSPHORYLASE (EC 2.4.1.1)
373	374	RXN02100	VW0318	2	2326	GLYCOTEN PHOSPHORYLASE (EC 2.4.1.1)
375	376	F RXA02100	GR00631	3	920	GLYCOTEN PHOSPHORYLASE (EC 2.4.1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOTEN PHOSPHORYLASE (EC 2.4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VW0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403	404	RXN01562	VW0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VW0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
413	414	RXN00043	VW0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417	418	RXN01752	VW0127	35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)
427	428	RXN03179	VW0336	2	667	URONATE ISOMERASE (EC 5.3.1.12)
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
431	432	RXN03180	VW0337	672	163	URONATE ISOMERASE (EC 5.3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00662	1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
437	438	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.4.0)
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	VV0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VV0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10556	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VV0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	VV0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	VV0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
469	470	RXN03030	VV0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	VV0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VV0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VV0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VV0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VV0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VV0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
483	484	RXN01593	VV0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VV0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VV0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233	GR00006	1417	260	protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

- 67 -

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
527	528	RXC01659				protein involved in sugar metabolism
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism
TCA-cycle						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VV0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VV0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VV0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	ACONITATE HYDRATASE (EC 4.2.1.3)
563	564	RXA01745	GR00495	2	1495	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
565	566	RXA00782	GR00206	3984	3103	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VV0139	11307	12806	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575	576	RXA00290	GR00046	4693	5655	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
577	578	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VV0066	2	583	MALIC ENZYME (EC 1.1.1.39)
585	586	RXN02046	VV0025	15056	14640	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587	588	RXN00389	VV0025	11481	9922	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)

Table 1 (continued)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1863	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
600	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylisocitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4.1.3.31)
619	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
625	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
631	634	RXN00317	VW0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VW0124	14236	14843	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Redox Chain

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
641	642	RXN01744	VW0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653	654	RXN02480	VW0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
665	666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN
667	668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
669	670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN
671	672	RXA01227	GR00355	1199	1519	FERREDOXIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN-NAD(+) REDUCTASE (EC 1.18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	F RXN00606	VW0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
685	686	RXN00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
687	688	RXN00595	VW0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VW0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VW0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	VW0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VW0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VW0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VW0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VW0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VW0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VW0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VW0317	3552	2794	Hypothetical Oxidoreductase
751	752	RXN02206	VW0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VW0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VW0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VW0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

- 71 -

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
767	768	RXN02821	VV0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VV0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
779	780	RXN00684	VV0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.--)
781	782	RXN00387	VV0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcjAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutarylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ001436			Wehrmann, A. et al. "Different modes of diaminoimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotin synthetase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and deshiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranyl synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

		Phosphoenolpyruvate carboxylase	
M25819			O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; clgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cgIIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

	bioB	Biotin synthase	
U31281			Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

	leuA	Isopropyl/malate synthase	
X70959			Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Elkman, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylmethionine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting <i>Arthrobacter aureus</i> C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	Moreau, S. et al. "Analysis of the integration functions of ϕ 304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y: cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y: cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rx000014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger naph, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rx000030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Unushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:A1497294	484	A1497294	fb63g03.y1 Zebrafish Washu MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOOO P80961 ANTIFREEZE PROTEIN LS-12. ; mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Unushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rx000032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinol transporter (dalT), D-arabinol kinase (dalK), D-arabinol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rx000041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rx000042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

rx000043	1287	GB_IN1:CEU33051 GB_PAT:126124 EM_PAT:E11760	4899 6911 6911	U33051 I26124 E11760	Caenorhabditis elegans sur-2 mRNA, complete cds. Sequence 4 from patent US 5556776. Base sequence of sucrase gene.	Caenorhabditis elegans Unknown. Corynebacterium glutamicum	40,276 97,591 97,591	23-Jan-96 07-OCT-1996 08-OCT-1997 (Rel. 52, Created) 24-Jun-98 19-Apr-97
rx000098	1743	GB_PR3:AC005174 GB_BA1:MSU88433	39769 1928	AC005174 U88433	Homo sapiens clone UWGC:g1584a012 from 7p14-15, complete sequence. Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	Homo sapiens Mycobacterium smegmatis	35,879 62,658	
rx000148	2334	GB_BA1:SC5A7 GB_BA1:MTCY10D7 GB_BA1:MTCY277	40337 39800 38300	AL031107 Z79700 Z79701	Streptomyces coelicolor cosmid 5A7. Mycobacterium tuberculosis H37Rv complete genome; segment 44/162. Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Streptomyces coelicolor Mycobacterium tuberculosis Mycobacterium tuberculosis	37,638 36,784 67,457	27-Jul-98 17-Jun-98 17-Jun-98
rx000149	1971	GB_BA1:MSGY456 GB_BA1:MSGY175 GB_BA1:MSGY456 GB_BA1:MSGY175	37316 18106 37316 18106	AD000001 AD000015 AD000001 AD000015	Mycobacterium tuberculosis sequence from clone y456. Mycobacterium tuberculosis sequence from clone y175. Mycobacterium tuberculosis sequence from clone y456. Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis	40,883 67,457 35,883 51,001	03-DEC-1996 10-DEC-1996 03-DEC-1996 10-DEC-1996
rx000195	684	GB_BA1:MTCY277 GB_BA1:MTCY274 GB_BA1:MSGB1529CS GB_BA1:MTCY274	38300 39991 36985 39991	Z79701 Z74024 L78824 Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162. Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Mycobacterium leprae cosmid B1529 DNA sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium tuberculosis	51,001 35,735 57,014 41,892	17-Jun-98 19-Jun-98 15-Jun-96 19-Jun-98
rx000196	738	GB_BA1:MTCY274 GB_BA1:MTCY274 GB_BA1:MTCY274	39991 39991 39991	Z74024 Z74024 Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Rat carbohydrate binding receptor gene, complete cds.	Mycobacterium tuberculosis Mycobacterium tuberculosis Rattus norvegicus	41,841 36,599 36,212	19-Jun-98 19-Jun-98 27-Apr-93
rx000202	1065	GB_EST11:AA253618 GB_EST26:A1390284 GB_EST26:A1390280	313 490 467	AA253618 A1390284 A1390280	Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence. mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' mRNA sequence. similar to TR:O09171 O09171 BETAIN-HOMOCYSTEINE METHYLTRANSFERASE; mRNA sequence. mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence.	Mus musculus Mus musculus Mus musculus	38,816 42,239 37,307	13-MAR-1997 2-Feb-99 2-Feb-99
rx000206	1161	GB_BA1:MLCB637 GB_BA1:MTV012	44882 70287	Z99263 AL021287	Mycobacterium leprae cosmid B637. Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium leprae Mycobacterium tuberculosis	58,312 36,632	17-Sep-97 23-Jun-99

Table 4 (continued)

rx00224	1074	GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
		GB_BA1:BUJ32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) and large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
		GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
		GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
rx00225	909	GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
		GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
		GB_EST31:A1676413	551	A1676413	etmEST0167 EtH1 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
rx00235	1398	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
		GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
		GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
rx00246	1158	GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 CompP (compP) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
		GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97
		GB_BA1:BACADHT	1688	D90421	B. stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,602	7-Feb-99
rx00251	831	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
rx00288	1134	GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999
		GB_GSS3:B16984	469	B16984	344A14.TVC CIT978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
rx00293	1035	GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpL34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
		GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94
GB_EST32:A1734238	512	A1734238	zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN); mRNA sequence.	Homo sapiens	41,502	14-Jun-99
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
GB_EST15:AA531468	414	AA531468	nj63d12.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
GB_VI:VARCG	186103	L22579	Varola major virus (strain Bangladesh-1975) complete genome.	Varola major virus	34,664	12-Jan-95
GB_VI:VWCGAA	185578	X69198	Varola virus DNA complete genome.	Varola virus	36,000	13-DEC-1996
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1998
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence.	Astasia longa	36,465	28-Jun-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
GB_EST23:A1120939	561	A1120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.	Mus musculus	41,113	2-Sep-98
GB_EST23:A1120939	561	A1120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.	Mus musculus	41,113	2-Sep-98
GB_EST32:A1726450	565	A1726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Homo sapiens	36,875	13-Sep-99
GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
GB_PR2:HSAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abliM, abliR genes and oriX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
rxa00517 1164	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS *** 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS *** 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_EST29:AI602158	481	AI602158	UI-R-ABO-vy-a-01-0-JI.s2 UI-R-ABO Rattus norvegicus cDNA clone UI-R-ABO-vy-a-01-0-JI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rxa00518 320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
rxa00606 2378	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
rxa00635 1860	GB_BA1:PAORF1	1440	X13378	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	53,912	14-Jul-95
rxa00679 1389	GB_PL2:AC010871	80381	AC010871	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	54,422	14-Jul-95
	GB_PL1:AT81KBGEN	81493	X98130	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
rxa00680 441	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
	GB_PR3:AC004058	38400	AC004058	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
	GB_PL1:AB026648	43481	AB026648	A thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
rxa00682 2022	GB_HTG3:AC010325	197110	AC010325	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete Arabidopsis thaliana sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS *** 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS *** 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rx00683	1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
		GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
		GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 311006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rx00686	927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_EST12:AA284399	431	AA284399	z557b04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rx00700	927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	41,943	2-Jul-99
		GB_EST25:AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	40,791	12-Nov-98
rx00703	2409	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
		GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rx00705	1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
		GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
		GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rx00782	1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
		GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
		GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rx00783	1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
rx00794	1128	GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene,pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
GB_PL2:AF016327	816	AF016327	Hordeum vulgare Barpermi1 (perm1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	63,101	17-Jun-98
GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
GB_PL1:SCSFAARP	7008	X68020	S.cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 81/162.	Mycobacterium tuberculosis	36,981	19-Jun-98
GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin.	Candida albicans	36,610	10-Apr-93
GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	51,586	12-MAY-1998
GB_BA1:RMPHA	7888	X93358	Rhizobium meliloti pha[A,B,C,D,E,F,G] genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralichthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralichthys olivaceus	41,640	28-Sep-99
GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK_44_Q_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99

Table 4 (continued)

GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone HRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***; 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
GB_EST18:AA709478	406	AA709478	v34a05.r1 Siratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***; 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***; 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
rx000965						
GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
GB_BA1:SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
GB_V1:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18:TR CIT-HSP Homo sapiens genomic clone 2318C18; genomic survey sequence.	Homo sapiens	36,528	14-Jul-98
rx01089 873						

Table 4 (continued)

GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17. TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18. TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
GB_BA1:CORPYKI	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
GB_GSS1:FR0005503	619	Z89313	F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98
GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92

rxa01200

Table 4 (continued)

rx01201 1764	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rx01202 1098	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
	GB_BA1:MCSQSSHC	5538	Y09978	M.capsulatus orf, orf, orf, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rx01204 933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999
rx01216 1124	GB_BA1:MTCY10G2	38970	Z82539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
	GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
	GB_BA1:CCRFLBDBA	4424	M69228	C.rescens flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rx01225 1563	GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
rx01227 444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996
rx01242 900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99

Table 4 (continued)

rx01243 1083	GB_GSS10:AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
rx01259 981	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,594	23-Nov-98
	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
rx01262 1284	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
rx01311 870	GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
	GB_BA1:D90841	20226	D90841	E.coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
rx01312 2142	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
rx01325 795	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
	GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
rx01332 576	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPC1-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
rx01332 576	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPC1-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPC111-375120, *** SEQUENCING IN PROGRESS ***; 25 Homo sapiens unordered pieces.	34,821	16-Sep-99
GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	58,487	19-OCT-1999
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	37,963	25-Feb-99
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	37,963	25-Feb-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	38,011	17-Jun-98
GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucumutase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	47,726	26-Apr-93
GB_GSS10:AQ194038	697	AQ194038	RPC111-47D24.TJ RPC11-11 Homo sapiens genomic clone RPC11-11-47D24, genomic survey sequence.	36,599	20-Apr-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	36,940	17-Jun-98
GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	35,284	14-MAY-1997
GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
GB_BA1:MTCV71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,778	10-Feb-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	32,658	16-Nov-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	38,395	16-Nov-99
GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4; putative transcriptional regulator, putative ferredoxin, putative cytochrome oxidoreductase, and putative oxidoreductase genes, complete unknown genes.	55,221	8-Jul-98
GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	100,000	24-Feb-97
GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPC111-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	36,756	30-Jan-99
GB_BA1:CGPTAACKA	3657	X89084	C. glutamicum pia gene and ackA gene.	100,000	23-MAR-1999
GB_BA1:D90861	14839	D90861	E. coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	53,041	29-MAY-1997
GB_PAT:E02087	1200	E02087	DNA encoding acetate kinase protein from Escherichia coli.	54,461	29-Sep-97
GB_GSS1:HPU60627	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	39,286	9-Apr-97
GB_EST31:A1701691	349	A1701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494, 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	39,412	3-Jun-99

Table 4 (continued)

rxα01478	1959	GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gb:L19886_mna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	Homo sapiens	39,574	14-Aug-97
		GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	16-Aug-99
		GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
rxα01482	1998	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
		GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,179	18-Jun-98
rxα01534								
rxα01535	1530	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	38,553	24-Jun-99
		GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
rxα01550	1635	GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	56,487	7-Feb-99
		GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
		GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (Glp1) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
rxα01562								
rxα01569	1482	GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
		GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	38,587	28-OCT-1998
		GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (picK) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
rxα01570	978	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98
		GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (mlb), glucose-1-phosphate thymidyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98

Table 4 (continued)

rx01571 723	GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rx01572 615	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rx01606 2799	GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
	GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
	GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
rx01626 468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
	GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
rx01632 1128	GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_GSS8:B99182	415	B99182	CIT-HSP-228013.TR CIT-HSP Homo sapiens genomic clone 228013, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
rx01633 1206	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	36,591	26-Nov-97
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

rx01695	1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
		GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
rx01702	1155	GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
		GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
rx01743	901	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
		GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
		GB_EST24-A1167112	579	A1167112	xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
		GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rx01744	1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
		GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
rx01745	836	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
rx01758	1140	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
		GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
		GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
		GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
rx01814	1785	GB_BA1:ABCCLEB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
rx01851	1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
		GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3-30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
		GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rx01859 1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
	GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPC193-25N14, *** SEQUENCING IN PROGRESS ***. 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rx01865 438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rx01882 1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
	GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-O4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
	GB_GSS3:BA2200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rx01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SC0001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
rx01886 897	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
	GB_GSS9:AQ116291	572	AQ116291	RPC111-49P6.TK.1 RPC1-11 Homo sapiens genomic clone RPC1-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***. 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***. 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwofii wzc, wzb, wza, weeA, weeB, weeC, wzc, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgj, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwofii	39,640	01-OCT-1999
rx01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC1-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***. 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99
GB_EST36:A1881527	598	A1881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, Zea mays mRNA sequence.		43,617	21-Jul-99
GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
GB_BA1:SCE63	37200	AL035840	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7q16 BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase. Arthrobacter sp.		56,283	04-MAY-1992
GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
GB_EST28:A1519629	612	A1519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgiA gene for phosphoglucosomerase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21); from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
GB_BA1:XSXCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21); from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rx02054	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
rx02056	GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
	GB_PAT:E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
	GB_BA1:DB4102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
	GB_BA1:MTV006	22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rx02061	GB_HTG7:AC005883	211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
	GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
rx02063	GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC F25118 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
	GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
	GB_GSS4:AQ687350	786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
	GB_EST38:AW028530	444	AW028530	ww27f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874 ; mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
rx02100	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
	GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism cluster1.	Streptomyces coelicolor	38,475	29-MAR-1999
	GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
rx02122	GB_EST37:AI948595	469	AI948595	wq07d12.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence.	Homo sapiens	37,259	6-Sep-99
	GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***; 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
rx02142	GB_RO:AF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***; 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***; 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_EST28:AI492095	485	AI492095	ig07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ; mRNA sequence.	Mus musculus	39,715	2-Jul-99
GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

Table 4 (continued)

rx02213 874	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoadyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998
rx02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds. Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
rx02256 1125	GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
	GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
	GB_BA1:CGGAPPGK	3804	X59403	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
rx02257 1338	GB_BA1:CGGAPPGK	3804	X59403	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
rx02258 900	GB_BA1:CGGAPPGK	3804	X59403	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
	GB_BA1:CORPEPC	4885	M25819	C-glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C-glutamicum ppv gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rx02259 2895	GB_BA1:CORPEPC	4885	M25819	C-glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C-glutamicum ppv gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

Table 4 (continued)

rx02288 969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12. complete sequence.	Homo sapiens	36,039	03-DEC-1999
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rx02292 798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
	GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99
	GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
rx02322 511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98
	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rx02326 939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	37,363	17-Jun-98
rx02327 1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98
rx02328 1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
rx02332 1266	GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
	GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cys) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
rx02333 1038	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
	GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99

Table 4 (continued)

GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
GB_BA1:CGACEA	2427	X75504	C-glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
GB_BA1:CGACEB	3024	X78491	C-glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,051	27-Apr-93
GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
GB_EST14:AA417723	374	AA417723	zv01b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element; contains element L1 repetitive element.; mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
GB_EST11:AA215428	303	AA215428	zf95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element.; mRNA sequence.	Homo sapiens	39,934	13-Aug-97
GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
GB_EST14:AA426336	375	AA426336	zv53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
GB_OM:BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

rx02485	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
	GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 37.	Aeropyrum pernix	48,014	22-Jun-99
rx02492	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
rx02528	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
	GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
rx02551	GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BACHUTWAP28954		D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BSGBGLUC	4290	Z34526	B. subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
rx02556	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
rx02560	GB_EST32:A1731605	566	A1731605	BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rx02572 668	GB_BA1:MTCV63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCV63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	19,820	29-Sep-99
rx02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rx02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rx02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rx02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amiR gene and cilE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:A1547662	377	A1547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rx02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
rx02654 1008	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rx02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	40,413	1-Jul-98
GB_BA1:PDENQO0URF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (birA) gene, complete cds.	Paracoccus denitrificans	40,735	20-MAY-1993
GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
GB_BA1:BACLDH	1147	M19394	B. caldolyticus lactate dehydrogenase (LDH) gene, complete cds.	Bacillus caldolyticus	57,371	26-Apr-93
GB_BA1:BACLDHL	1361	M14788	B. stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	57,277	26-Apr-93
GB_PAT:A06664	1350	A06664	B. stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfs Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	50,746	27-Jun-97
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfs Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	36,364	27-Jun-97
GB_EST19:AA758660	233	AA758660	ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	Homo sapiens	37,059	29-DEC-1998
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfs Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	42,149	27-Jun-97
GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655	15-Nov-99
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99

Table 4 (continued)

rx02740 1053	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573	01-MAR-1994
rx02741 1089	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
	GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 87 unordered pieces.	Drosophila melanogaster	38,728	20-Sep-99
	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
rx02743 1161	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
	GB_IN1:AB006546	931	AB006546	Ephydata fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydata fluviatilis	36,379	23-Jun-99
	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
rx02797 1028	GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	37,128	26-Jun-99
	GB_BA1:CGBETPGEN	2339	X93514	C-glutamicum betP gene.	Corynebacterium glutamicum	38,889	8-Sep-97
	GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321	08-OCT-1998
rx02803 680	GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
	GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MraA (mraA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	Pseudomonas syringae pv. syringae	50,445	9-Apr-97
rx02821 363	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314	20-Aug-98
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***; 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***; 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
	GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone Mus musculus 2610200J17, mRNA sequence.	Mus musculus	40,157	30-Jun-99

Table 4 (continued)

rx02829	373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS386 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216	1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPC1-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
		GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element; contains element HGR repetitive element ., mRNA sequence.	Homo sapiens	37,260	9-Nov-97
		GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5' mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215	1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
		GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
		GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224	1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
		GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
		GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* 10 (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & 15 Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Loris6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome 25 Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

30 *In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, *mutHLS*, *mutD*, *mutT*, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

- (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the
- 5 binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.
- 10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which
- 15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

- Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der
- 25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose,
- 30 ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

10 For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance

15 of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates

20 (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

25

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

30 within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- 25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

- 127 -

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on
5 a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule
10 to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical*
15 *Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994)
20 *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.*
25 (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between
30 two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

- 128 -

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid
5 molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped
10 BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-
15 17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described
20 in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap
25 weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present
30 in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

- 129 -

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

- 130 -

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, e.g., Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (e.g., mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, e.g., during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (e.g., in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of
5 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

- 135 -

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 5 18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.
- 10 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1,
- 15 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 20 22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 30 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

- 137 -

sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,
20 *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
Brevibacterium healii, *Brevibacterium ketoglutamicum*, *Brevibacterium*
25 *ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

- 138 -

and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

5 32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

15

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1,
20 thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the
25 Sequence Listing, wherein the nucleic acid molecule is disrupted.

35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more
30 nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

- 139 -

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified
- 5 relative to the wild-type regulatory region of the molecule.

SEQUENCE LASTING

<110> BASF Aktiengesellschaft
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION
<130> BGI-126CPPC
<140>
<141>
<160> 782

<210> 1
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXS02735

<400> 1
gaggagcttc gccacatgga tccagatttg ggctaccagc acgcactatc cggcttgtcc 60
agcgtcaagc tggaaccgt ctaaggagaa atacaacact atg gtt gat gta gta 115
Met Val Asp Val Val
1 5
cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc 163
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe
10 15 20
att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta 211
Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
25 30 35
gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc 259
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
40 45 50
gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly
55 60 65
gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag 355
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln
70 75 80 85
gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att 403
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile
90 95 100
cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct 451
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
105 110 115
tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac 499
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
120 125 130
ctg ctc ggc atg qgt qgc gaa qgc cat atc aac tcc ctg ttc cct cac 547

```

Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His
135                      140                      145

acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat    595
Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp
150                      155                      160                      165

tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt    643
Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val
170                      175                      180

cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct    691
His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
185                      190                      195

gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct    739
Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro
200                      205                      210

gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat    787
Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp
215                      220                      225

gat gct gca gga aat ctc taagcagcgc cagctctaac aag                828
Asp Ala Ala Gly Asn Leu
230                      235

```

<210> 2
 <211> 235
 <212> PRT
 <213> *Corynebacterium glutamicum*

```

<400> 2
Met Val Asp Val Val Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln
1                      5                      10                      15

Ala Ala Ser Lys Phe Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn
20                      25                      30

Gly Thr Ala Gln Val Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu
35                      40                      45

Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
50                      55                      60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
65                      70                      75                      80

Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
85                      90                      95

Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
100                      105                      110

Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
115                      120                      125

Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
130                      135                      140

```

Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
 145 150 155 160
 Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
 165 170 175
 Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
 180 185 190
 Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
 195 200 205
 Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val
 210 215 220
 Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
 225 230 235

<210> 3

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA01626

<400> 3

gcaatagcga atgcgtaatt aaccacactt caaacctagc ccctcaggtg gaggattccg 60

acattaccgt ctgaaaaatt tcatccgtag gctaaagagc atg tcg aaa acg atc 115
 Met Ser Lys Thr Ile
 1 5

atc gtg cgc acc gaa att gaa atc cct gga cac cca acc gcc atc cat 163
 Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His Pro Thr Ala Ile His
 10 15 20

atc gca gag atg cag gag ctt ccc cca tct gag gct caa ggc ggc gtg 211
 Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu Ala Gln Gly Gly Val
 25 30 35

cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259
 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
 40 45 50

ggg gat gtc gtt act ggt gca ggt gtt att ggc gga tct aat ttc cag 307
 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln
 55 60 65

ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355
 Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala
 70 75 80 85

gat ttc ccc gat atc aag gcg gtt gtt atc tcc gcg gag act ttt gaa 403
 Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu
 90 95 100

ggc ctg tgg ctg gaa gcg gga gcg aag ttc cct ggg tta aat 445

Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro Gly Leu Asn
 105 110 115

taaccacttg cagtataccc tag

468

<210> 4

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 4

Met Ser Lys Thr Ile Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His
 1 5 10 15

Pro Thr Ala Ile His Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu
 20 25 30

Ala Gln Gly Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu
 35 40 45

Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly
 50 55 60

Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
 65 70 75 80

Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser
 85 90 95

Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro
 100 105 110

Gly Leu Asn
 115

<210> 5

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA02245

<400> 5

gccacaccgc caccggcaccg atgcgatggt tgtggcagtg ctgcgaaaga agtagacctg 60

tgagctaagt ggggtagaca agagggctat gatttagggc atg gca caa cgt act 115
 Met Ala Gln Arg Thr
 1 5

cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg 163
 Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
 10 15 20

gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc 211
 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
 25 30 35

atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca 259
 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
 40 45 50

gct gcg gtc aac cgc gtt acg gac aaa gaa cta gac gtc cac ctg atg 307
 Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met
 55 60 65

atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg 355
 Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
 70 75 80 85

gac tgc att gtt ttc cac gtt gaa gcc acc gaa ggt cac gtt gag ttg 403
 Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
 90 95 100

gct aag tac atc cgt tcc aag ggt gtg cgt gca ggt ttc tcc ctg cgc 451
 Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg
 105 110 115

cct gga act ccc atc gag gat tac ttg gat gac ctc gag cac ttc gat 499
 Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
 120 125 130

gaa gtc atc gtc atg agc gtc gag cct gga ttc ggt ggc caa agc ttc 547
 Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe
 135 140 145

atg cct gaa caa ctg gaa aag gtt cgt acc ctg cgc aag gtc atc gat 595
 Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp
 150 155 160 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc 643
 Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala
 170 175 180

aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
 185 190 195

ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag 739
 Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu
 200 205 210

ttg cga gca ctc gcg cag taaatggatg ttgcgcacgc gtt 780
 Leu Arg Ala Leu Ala Gln
 215

<210> 6

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Met Ala Gln Arg Thr Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp
 1 5 10 15

Phe Ser Arg Leu Gly Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp
 20 25 30

Ile His Val Asp Ile Met Asp Gly His Phe Val Pro Asn Leu Ser Phe
 35 40 45
 Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
 50 55 60
 Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
 65 70 75 80
 Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
 85 90 95
 Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
 100 105 110
 Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
 115 120 125
 Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
 130 135 140
 Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
 145 150 155 160
 Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
 165 170 175
 Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
 180 185 190
 Asp Ala Phe Val Ala Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn
 195 200 205
 Lys Ala Ile Gln Glu Leu Arg Ala Leu Ala Gln
 210 215

<210> 7

<211> 442

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXA01015

<400> 7

ccaagattga gtcgagctat tttgcgattt gtgaaccccc aaatagggga aaagtccggg 60

tatccgccgt tgtgaaaatg cctgcagtaa actgacttcc atg cgc gta tac ctt 115
 Met Arg Val Tyr Leu
 1 5

gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac 163
 Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His
 10 15 20

ctt aag gcc cac ggc cac gaa gtg atc gac tgc gga gcc cac acc tat 211
 Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr

	25	30	35	
gat gca gaa gat gac tac cca gcc ttc tgc atc gaa gca gct agc cgc				259
Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile Glu Ala Ala Ser Arg				
	40	45	50	
aca gta aac gac cca ggc tca ctc ggc atc gtc ctg ggt gga tcc gga				307
Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly				
	55	60	65	
aac ggc gag cag atc gcc gcc aac aag gtc aag ggt gca cgt tgt gca				355
Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala				
	70	75	80	85
ctt gct tgg tct gtt gaa act gca cgc ctc gcc cgc gag cac aac aat				403
Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn				
	90	95	100	
gcg aac ctc atc ggc atc ggc ggc cgc atg cac tca gag				442
Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His Ser Glu				
	105	110		

<210> 8

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Met Arg Val Tyr Leu Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn	
1 5 10 15	

Ala Ile Ala Glu His Leu Lys Ala His Gly His Glu Val Ile Asp Cys	
20 25 30	

Gly Ala His Thr Tyr Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile	
35 40 45	

Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val	
50 55 60	

Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys	
65 70 75 80	

Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala	
85 90 95	

Arg Glu His Asn Asn Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His	
100 105 110	

Ser Glu

<210> 9

<211> 2142

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2119)

<223> RXN01312

<400> 9

```

gcagttgcgt acatcgttcc tgcactgggtc ctgatcggca acatcaccat tccgttcgcc 60

atcgcctgttg gttggattgc gtaaagggtta ggaagaattt atg agc act cac tct 115
                                         Met Ser Thr His Ser
                                         1           5

gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag 163
Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
                        10                        15                        20

gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211
Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
                        25                        30                        35

acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
                        40                        45                        50

cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg 307
Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
                        55                        60                        65

tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc 355
Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
70                        75                        80                        85

aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct 403
Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
                        90                        95                        100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac 451
Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
105                        110                        115

ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt 499
Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
120                        125                        130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc 547
Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
135                        140                        145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt 595
Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
150                        155                        160                        165

ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
170                        175                        180

tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca 691
Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
185                        190                        195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
200                        205                        210

```


cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag	787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys	
215 220 225	
cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc	835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr	
230 235 240 245	
gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac	883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn	
250 255 260	
gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc	931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile	
265 270 275	
atg cgt gca tac gaa gcc ggc gca tac ttc gcg tcc cca tcg ttc atc	979
Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile	
280 285 290	
cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag	1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys	
295 300 305	
acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc	1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser	
310 315 320 325	
cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat	1123
Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp	
330 335 340	
gag cgc gac tac ttc ctg gag cgc cgc tac cca gca ttc ggt aac ctc	1171
Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu	
345 350 355	
gtc cca cgt gac gtt gct tcc cgt gcg atc tcc cag cag atc aat gct	1219
Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala	
360 365 370	
ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc	1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg	
375 380 385	
gac gcc acc gag cgc ctc gga cag gac acc atc cgc gag cgt tac tcc	1315
Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser	
390 395 400 405	
aac ctc ttc acc atg tac gaa gag gca att ggc gag gac cca tac tcc	1363
Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser	
410 415 420	
agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc	1411
Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu	
425 430 435	
tgg act gac ttc aac gaa atg acg tca ctc cca ggt ctg ttc tgc gca	1459
Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala	
440 445 450	

ggc gaa gca tcc tgg acc tac cac ggt gca aac cgt ctg ggc gca aac 1507
 Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn
 455 460 465

tcc ctg ctc tcc gct tcc gtc gat ggc tgg ttc acc ctg cca ttc acc 1555
 Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
 470 475 480 485

atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag 1603
 Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
 490 495 500

gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att 1651
 Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
 505 510 515

gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac 1699
 Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
 520 525 530

gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc 1747
 Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
 535 540 545

tgt ggc gtt tcc cga aac gta gaa gac ctc cag gat ggc atc aac aag 1795
 Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
 550 555 560 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc 1843
 Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly
 570 575 580

agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc 1891
 Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
 585 590 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc 1939
 Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
 600 605 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat 1987
 Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp
 615 620 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg 2035
 Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp
 630 635 640 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc 2083
 Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
 650 655 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact 2129
 Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr Lys
 665 670

tacacttgag atc 2142

<210> 10

<211> 673

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

```

Met Ser Thr His Ser Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val
 1           5           10           15

Ser Val Leu Pro Glu Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu
          20           25           30

Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
          35           40           45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
 50           55           60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu
 65           70           75           80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
          85           90           95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
          100          105          110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
          115          120          125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
 130          135          140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
 145          150          155          160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
          165          170          175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
          180          185          190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
          195          200          205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
 210          215          220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
 225          230          235          240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
          245          250          255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
          260          265          270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
          275          280          285

Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
          290          295          300

```

Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp
 305 310 315 320
 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
 325 330 335
 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
 340 345 350
 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
 355 360 365
 Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
 370 375 380
 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
 385 390 395 400
 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
 405 410 415
 Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
 420 425 430
 Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
 435 440 445
 Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
 450 455 460
 Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
 465 470 475 480
 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
 485 490 495
 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
 500 505 510
 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
 515 520 525
 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
 530 535 540
 Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
 545 550 555 560
 Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
 565 570 575
 Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
 580 585 590
 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
 595 600 605
 Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
 610 615 620
 His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys

625											630											635											640
Phe	Val	Ser	Ala	Trp	Glu	Pro	Gly	Glu	Asn	Gly	Thr	Phe	Val	Cys	His																		
				645					650					655																			
Ala	Glu	Pro	Leu	Phe	Phe	Glu	Ser	Val	Pro	Leu	Gln	Thr	Arg	Asn	Tyr																		
			660				665				670																						
Lys																																	
<210> 11																																	
<211> 1100																																	
<212> DNA																																	
<213> Corynebacterium glutamicum																																	
<220>																																	
<221> CDS																																	
<222> (1)..(1077)																																	
<223> FRXA01312																																	
<400> 11																																	
gag	tcg	ctg	cgt	aac	gac	ggc	cgc	atc	tgg	tcc	cct	aag	gaa	ccg	aac	48																	
Glu	Ser	Leu	Arg	Asn	Asp	Gly	Arg	Ile	Trp	Ser	Pro	Lys	Glu	Pro	Asn																		
1				5				10				15																					
gat	aac	cgc	gat	cca	aac	acc	atc	cct	gag	gat	gag	cgc	gac	tac	ttc	96																	
Asp	Asn	Arg	Asp	Pro	Asn	Thr	Ile	Pro	Glu	Asp	Glu	Arg	Asp	Tyr	Phe																		
			20				25				30																						
ctg	gag	cgc	cgc	tac	cca	gca	ttc	ggg	aac	ctc	gtc	cca	cgt	gac	gtt	144																	
Leu	Glu	Arg	Arg	Tyr	Pro	Ala	Phe	Gly	Asn	Leu	Val	Pro	Arg	Asp	Val																		
			35				40				45																						
gct	tcc	cgt	gcg	atc	tcc	cag	cag	atc	aat	gct	ggg	ctc	ggg	gtt	gga	192																	
Ala	Ser	Arg	Ala	Ile	Ser	Gln	Gln	Ile	Asn	Ala	Gly	Leu	Gly	Val	Gly																		
			50				55				60																						
cct	ctg	aac	aac	gct	gca	tac	ctg	gac	ttc	cgc	gac	gcc	acc	gag	cgc	240																	
Pro	Leu	Asn	Asn	Ala	Ala	Tyr	Leu	Asp	Phe	Arg	Asp	Ala	Thr	Glu	Arg																		
			65				70				75				80																		
ctc	gga	cag	gac	acc	atc	cgc	gag	cgt	tac	tcc	aac	ctc	ttc	acc	atg	288																	
Leu	Gly	Gln	Asp	Thr	Ile	Arg	Glu	Arg	Tyr	Ser	Asn	Leu	Phe	Thr	Met																		
				85				90				95																					
tac	gaa	gag	gca	att	ggc	gag	gac	cca	tac	tcc	agc	cca	atg	cgt	att	336																	
Tyr	Glu	Glu	Ala	Ile	Gly	Glu	Asp	Pro	Tyr	Ser	Ser	Pro	Met	Arg	Ile																		
			100				105				110																						
gca	ccg	acc	tgc	cac	ttc	acc	atg	ggg	ggc	ctc	tgg	act	gac	ttc	aac	384																	
Ala	Pro	Thr	Cys	His	Phe	Thr	Met	Gly	Gly	Leu	Trp	Thr	Asp	Phe	Asn																		
			115				120				125																						
gaa	atg	acg	tca	ctc	cca	ggg	ctg	ttc	tgc	gca	ggc	gaa	gca	tcc	tgg	432																	
Glu	Met	Thr	Ser	Leu	Pro	Gly	Leu	Phe	Cys	Ala	Gly	Glu	Ala	Ser	Trp																		
			130				135				140																						
acc	tac	cac	ggg	gca	aac	cgt	ctg	ggc	gca	aac	tcc	ctg	ctc	tcc	gct	480																	
Thr	Tyr	His	Gly	Ala	Asn	Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	Ser	Ala																		

145	150	155	160	
tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctc				528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu	165	170	175	
ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca				576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala	180	185	190	
cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc				624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly	195	200	205	
aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac				672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr	210	215	220	
cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga				720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg	225	230	235	240
aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc				768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu	275	280	285	
ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc				912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg	305	310	315	320
gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat				1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro	340	345	350	
ctg cag aca agg aac tac aag taatgaaact tacacttgag atc				1100
Leu Gln Thr Arg Asn Tyr Lys	355			

<210> 12

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
 1 5 10 15
 Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
 20 25 30
 Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
 35 40 45
 Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
 50 55 60
 Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
 65 70 75 80
 Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
 85 90 95
 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
 100 105 110
 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
 115 120 125
 Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
 130 135 140
 Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
 145 150 155 160
 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
 165 170 175
 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
 180 185 190
 Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
 195 200 205
 Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
 210 215 220
 His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
 225 230 235 240
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
 245 250 255
 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
 260 265 270
 Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
 275 280 285
 Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
 290 295 300
 Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
 305 310 315 320
 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn

[illegible]

gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg	595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met	
150 155 160 165	
gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg	643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val	
170 175 180	
ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag	691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln	
185 190 195	
acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc	739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser	
200 205 210	
ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc	787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg	
215 220 225	
ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg	835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu	
230 235 240 245	
ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt	883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly	
250 255 260	
ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg	931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala	
265 270 275	
atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc	979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys	
280 285 290	
acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc	1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe	
295 300 305	
ggc cgt cgc ttc gct gcc cgc ctt gaa gag caa gtc cta ggc aac ggc	1075
Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly	
310 315 320 325	
ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga	1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg	
330 335 340	
gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc	1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr	
345 350 355	
gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa	1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu	
360 365 370	
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa	1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu	
375 380 385	

gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa 1315
 Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
 390 395 400 405

 gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat 1363
 Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
 410 415 420

 gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc 1411
 Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
 425 430 435

 gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct 1459
 Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
 440 445 450

 gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt 1507
 Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
 455 460 465

 ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg 1555
 Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
 470 475 480 485

 gat cct tac gcc ggc tagcatctgc ccctttacaa atc 1593
 Asp Pro Tyr Ala Gly
 490

<210> 14

<211> 490

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 14

Met Thr Ile Asn Val Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu
 1 5 10 15

 Leu Ile Gly Asp Ser Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp
 20 25 30

 Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
 35 40 45

 Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
 50 55 60

 Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65 70 75 80

 Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
 85 90 95

 Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
 100 105 110

 Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
 115 120 125

 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
 130 135 140

Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
 145 150 155 160
 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
 165 170 175
 Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
 180 185 190
 Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
 195 200 205
 Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
 210 215 220
 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
 225 230 235 240
 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
 245 250 255
 Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
 260 265 270
 Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
 275 280 285
 Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
 290 295 300
 Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
 305 310 315 320
 Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
 325 330 335
 Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
 340 345 350
 Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
 355 360 365
 Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
 370 375 380
 Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
 385 390 395 400
 Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
 405 410 415
 Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
 420 425 430
 Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
 435 440 445
 Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
 450 455 460

Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln
 465 470 475 480

Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
 485 490

<210> 15

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01311

<400> 15

tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

tcttcgaatc tgtccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70 75 80 85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
 Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
 90 95 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
 105 110 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
 120 125 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595

Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
 230 235 240 245

ggc aaa gac gac tagtctttaa tccaagtaag tac 870
 Gly Lys Asp Asp

<210> 16

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
 1 5 10 15

Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
 20 25 30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
 35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
 245

<210> 17
 <211> 1530
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1507)
 <223> RXA01535

<400> 17
 acccacctca ctctaggggt ggactccagt gtttcgcgac aacacaatga gtaagcttgt 60

gacagccgta tttaattctc agtaagaaat gagtgatttc atg acc gag cag gaa 115
 Met Thr Glu Gln Glu
 1 5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
 10 15 20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
 25 30 35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
 40 45 50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
 55 60 65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
 70 75 80 85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
 Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly

90								95				100				
act	tcc	tcc	aac	atg	aac	acc	aat	gag	gtt	atc	gct	tcc	atc	gcg	aag	451
Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	Ala	Ser	Ile	Ala	Lys	
			105					110					115			
gct	aac	ggc	ggt	gag	ggt	cac	cca	aat	gac	cac	gtc	aac	atg	ggg	cag	499
Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln	
		120					125					130				
tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	ggt	gct	gca	acc	gaa	547
Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His	Val	Ala	Ala	Thr	Glu	
		135				140					145					
gct	gct	gtc	aat	gac	ctc	atc	cca	ggc	ctg	aag	ggt	ctg	cac	gag	tct	595
Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	Val	Leu	His	Glu	Ser	
150					155					160					165	
ttg	gcg	aag	aag	gct	aac	gag	tgg	tct	gag	ggt	ggt	aag	tcc	ggc	cgc	643
Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	Val	Lys	Ser	Gly	Arg	
				170					175					180		
acc	cac	ctg	atg	gac	gct	ggt	cca	gta	acc	ctg	ggc	cag	gag	ttc	ggg	691
Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly	
			185					190					195			
ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	cgc	ggt	gag	gct	act	739
Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	Arg	Val	Glu	Ala	Thr	
		200					205					210				
ctt	cct	cgc	ctt	ggt	gag	ctg	gct	att	ggt	ggc	acc	gct	gct	ggg	acc	787
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr	
		215				220					225					
ggt	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	ggt	ggt	gct	gaa	ctg	835
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu	
230					235					240					245	
atc	aac	ttg	acc	gac	gtc	aag	gag	ctc	aag	gaa	gct	gag	aac	cac	ttc	883
Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe	
				250					255					260		
gag	gct	cag	gct	gca	cgc	gac	gct	ctt	ggt	gag	ttc	tcc	ggc	gca	atg	931
Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met	
			265					270					275			
cgc	ggt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
		280					285					290				
atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027
Met	Gly	Ser	Gly</													

gct gtt gcg ttc tcc ggc acc cag ggc cag ttc gag ctc aac gtg ttc 1171
 Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe
 345 350 355

 atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct 1219
 Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
 360 365 370

 aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca 1267
 Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
 375 380 385

 aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt 1315
 Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
 390 395 400 405

 acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct 1363
 Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
 410 415 420

 aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat 1411
 Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
 425 430 435

 ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag 1459
 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
 440 445 450

 cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
 Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
 455 460 465

 taaaactaga acccgataaa taa 1530

<210> 18

<211> 469

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 18

Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr Met Gly Glu Val
 1 5 10 15

Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val
 20 25 30

Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
 35 40 45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
 50 55 60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
 65 70 75 80

Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
 85 90 95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile

100					105					110					
Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His
		115					120					125			
Val	Asn	Met	Gly	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His
		130					135					140			
Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys
		145					150					155			
Val	Leu	His	Glu	Ser	Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val
				165					170					175	
Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu
				180					185					190	
Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu
		195					200					205			
Arg	Val	Glu	Ala	Thr	Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly
		210					215					220			
Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys
		225					230					235			
Val	Val	Ala	Glu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu
				245					250					255	
Ala	Glu	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu
				260					265					270	
Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala
		275							280					285	
Asn	Asp	Ile	Arg	Leu	Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu
		290							295					300	
Ile	Arg	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys
		305							310					315	
Val	Asn	Pro	Val	Leu	Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val
				325					330					335	
Ile	Gly	Asn	Asp	Ala	Ala	Val	Ala	Phe	Ser	Gly	Thr	Gln	Gly	Gln	Phe
				340					345					350	
Glu	Leu	Asn	Val	Phe	Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser
		355							360					365	
Ala	Arg	Leu	Leu	Ala	Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val
		370							375					380	
Asp	Gly	Ile	Glu	Pro	Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser
		385							390					395	
Ser	Pro	Ser	Ile	Val	Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr	Glu	Ala
				405					410					415	
Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	Leu	Ala	Glu	Gly	Lys	Thr	Ile	Arg
				420					425					430	

Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
 435 440 445

Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
 450 455 460

Arg Glu Asn Lys Phe
 465

<210> 19

<211> 1164

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1141)

<223> RXA00517

<400> 19

ggctcttagaa ccagcgtgca ctgatggcga ttaaaggggg ttgcgcctat acctattgct 60

gggtatacatt tcggtataacc taaaccgaat tgaggggattc atg cca gaa gtc act 115
 Met Pro Glu Val Thr
 1 5

gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163
 Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
 10 15 20

act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211
 Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
 25 30 35

cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259
 Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
 40 45 50

tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac 307
 Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
 55 60 65

gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac 355
 Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
 70 75 80 85

aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg 403
 Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
 90 95 100

act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc 451
 Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
 105 110 115

aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa 499
 Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
 120 125 130

gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc 547

Gly	Cys	Val	Ser	Ile	Leu	Thr	Thr	Asn	Ala	Ser	Pro	Ala	Met	Ala	Pro		
135						140					145						
tgg	ggt	ggc	aga	gaa	aaa	cgg	atc	ggt	acc	aac	cca	tgg	tct	att	gcg	595	
Trp	Gly	Gly	Arg	Glu	Lys	Arg	Ile	Gly	Thr	Asn	Pro	Trp	Ser	Ile	Ala		
150					155					160					165		
gca	cct	ttt	gga	gaa	acg	gct	acg	gta	gtc	gat	ata	gcc	aat	act	gcg	643	
Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp	Ile	Ala	Asn	Thr	Ala		
				170					175					180			
gtt	gcg	cgc	gga	aag	atc	tac	cac	gca	cga	cag	aca	aac	atg	ccc	att	691	
Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln	Thr	Asn	Met	Pro	Ile		
			185					190					195				
cct	gag	act	tgg	gcg	atc	acg	agt	gag	ggc	gca	ccc	acc	acg	gat	cct	739	
Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala	Pro	Thr	Thr	Asp	Pro		
		200					205					210					
gct	gag	gca	atc	aac	ggt	gtc	gtc	ctt	ccc	atg	gct	ggt	cac	aaa	ggt	787	
Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met	Ala	Gly	His	Lys	Gly		
	215					220					225						
tat	gcg	att	agc	ttc	atg	atg	gat	gtg	ctt	tct	gga	gtt	ctc	act	ggt	835	
Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser	Gly	Val	Leu	Thr	Gly		
230					235					240					245		
tcc	cag	cac	agc	acc	aag	gta	cat	ggt	ccg	tat	gat	ccc	act	ccc	cca	883	
Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr	Asp	Pro	Thr	Pro	Pro		
				250					255					260			
ggt	gga	gct	ggc	cac	ttg	ttc	atc	gcg	ttg	gat	gtt	gca	gcg	ttt	cgc	931	
Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp	Val	Ala	Ala	Phe	Arg		
			265					270					275				
gat	cca	caa	gat	ttc	gat	gac	gca	ctc	agc	gat	ctg	gtt	ggg	gaa	gtt	979	
Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp	Leu	Val	Gly	Glu	Val		
		280					285					290					
aaa	tcc	act	ccg	aaa	gca	caa	aac	acc	gag	gag	att	ttc	tac	ccc	ggt	1027	
Lys	Ser	Thr	Pro	Lys	Ala	Gln	Asn	Thr	Glu	Glu	Ile	Phe	Tyr	Pro	Gly		
		295				300					305						
gaa	tcg	gaa	gac	cgt	gcg	cat	cgg	aaa	aac	tct	gcg	cac	ggt	att	tca	1075	
Glu	Ser	Glu	Asp	Arg	Ala	His	Arg	Lys	Asn	Ser	Ala	His	Gly	Ile	Ser		
310					315					320					325		
ttg	cct	gaa	aaa	acg	tgg	atg	gaa	ctg	caa	gaa	ctg	gca	atc	gag	aac	1123	
Leu	Pro	Glu	Lys	Thr	Trp	Met	Glu	Leu	Gln	Glu	Leu	Ala	Ile	Glu	Asn		
				330					335					340			
cat	gtt	gta	act	cac	cgt	tgatctgcgc	gttaaacctg	gcc								1164	
His	Val	Val	Thr	His	Arg												
				345													

<210> 20

<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Met Pro Glu Val Thr Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr
 1 5 10 15
 Asp Ile Leu Thr Lys Thr Gly Val Pro Ala Ala Asp Ala His Leu Val
 20 25 30
 Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
 35 40 45
 Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
 50 55 60
 Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
 65 70 75 80
 Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
 85 90 95
 Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
 100 105 110
 Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
 115 120 125
 Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
 130 135 140
 Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
 145 150 155 160
 Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
 165 170 175
 Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
 180 185 190
 Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
 195 200 205
 Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
 210 215 220
 Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
 225 230 235 240
 Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
 245 250 255
 Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
 260 265 270
 Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
 275 280 285
 Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
 290 295 300
 Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
 305 310 315 320

Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu
 325 330 335

Leu Ala Ile Glu Asn His Val Val Thr His Arg
 340 345

<210> 21

<211> 1107

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1084)

<223> RXA01350

<400> 21

tgcagtatcg tcaagatcac ccaaaactgg tggctgttct cttttaagcg ggatagcatg 60

ggttcttaga ggacccccta caaggattga ggattgttta atg aat tcc ccg cag 115
 Met Asn Ser Pro Gln
 1 5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163
 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
 10 15 20

tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc 211
 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
 25 30 35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
 Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
 40 45 50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc 307
 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
 55 60 65

ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc 355
 Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
 70 75 80 85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403
 Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
 90 95 100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451
 Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
 105 110 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt 499
 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
 120 125 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547
 Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
 135 140 145

cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac 595

Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
 150 155 160 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg 643
 Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
 170 175 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc 691
 Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
 185 190 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg 739
 Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
 200 205 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac 787
 Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
 215 220 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct 835
 Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
 230 235 240 245

gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc 883
 Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
 250 255 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att 931
 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
 265 270 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag 979
 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
 280 285 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc 1027
 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075
 Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
 310 315 320 325

gac ttg ctc taatctttaa cgcatgactt cgc 1107
 Asp Leu Leu

<210> 22

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Met Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly
 1 5 10 15

Ala Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly
 20 25 30

Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile

35	40	45
Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp 50 55 60		
Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn 65 70 75 80		
Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro 85 90 95		
Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys 100 105 110		
Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp 115 120 125		
Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile 130 135 140		
Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met 145 150 155 160		
Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu 165 170 175		
Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His 180 185 190		
Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu 195 200 205		
Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile 210 215 220		
Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys 225 230 235 240		
Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp 245 250 255		
Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr 260 265 270		
Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val 275 280 285		
Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp 290 295 300		
Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu 305 310 315 320		
Arg Glu Ala Val Arg Asp Leu Leu 325		

<210> 23

<211> 1092

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1069)

<223> RXA02149

<400> 23

ttgcagagtg aaccacgatg atggttggac agctgttgat agctaactctt tgaaagatta 60

aattcaccta aatcctgtgt agaacgcgag gggcactctt atg cca caa aaa ccg 115
 Met Pro Gln Lys Pro
 1 5

gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc 163
 Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
 10 15 20

ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg 211
 Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
 25 30 35

tcg ccg cgc acg acg cag gca atg gaa cag ggc att ttt gat cta gtc 259
 Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
 40 45 50

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc 307
 Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val
 55 60 65

gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac 355
 Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His
 70 75 80 85

ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg 403
 Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
 90 95 100

ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt 451
 Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
 105 110 115

gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg 499
 Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
 120 125 130

gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att 547
 Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
 135 140 145

tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt 595
 Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
 150 155 160 165

gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag 643
 Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
 170 175 180

cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct 691
 Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
 185 190 195

tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc 739
 Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala
 200 205 210

gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa 787
 Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
 215 220 225

gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835
 Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
 230 235 240 245

ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc 883
 Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
 250 255 260

atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc 931
 Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
 265 270 275

tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct 979
 Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
 280 285 290

ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc 1027
 Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile
 295 300 305

ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac 1069
 Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn
 310 315 320

taggtgtttt tcggtgggct gcg 1092

<210> 24

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

Met Pro Gln Lys Pro Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly
 1 5 10 15

Thr Asn Met Arg Ala Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr
 20 25 30

Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly
 35 40 45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
 50 55 60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65 70 75 80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
 85 90 95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
 100 105 110

Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
 115 120 125
 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
 130 135 140
 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
 145 150 155 160
 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
 165 170 175
 Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
 180 185 190
 Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
 195 200 205
 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
 210 215 220
 Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
 225 230 235 240
 Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
 245 250 255
 Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
 260 265 270
 Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
 275 280 285
 Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
 290 295 300
 Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val
 305 310 315 320
 Glu Ala Asn

<210> 25
 <211> 1785
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1762)
 <223> RXA01814

<400> 25
 tgtaaagcca ccctactccg tgaattttgc cgtatctcgt gcgcacaatt gcttttgagg 60
 ggaagatgaa gagaaagtat tgggtgtttta aggagcaaac atg gca cat gaa cgc 115
 Met Ala His Glu Arg
 1 5

gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg 163
 Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu
 10 15 20

gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag 211
 Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln
 25 30 35

cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc 259
 Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser
 40 45 50

gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac 307
 Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp
 55 60 65

tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc 355
 Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly
 70 75 80 85

cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag 403
 Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu
 90 95 100

gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc 451
 Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg
 105 110 115

tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat 499
 Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp
 120 125 130

ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc 547
 Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly
 135 140 145

atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa 595
 Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys
 150 155 160 165

tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg 643
 Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp
 170 175 180

atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg 691
 Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val
 185 190 195

aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac 739
 Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr
 200 205 210

gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc 787
 Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile
 215 220 225

gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt 835
 Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly
 230 235 240 245

ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc 883

Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	Glu	Thr	His	Gly	Leu	
				250					255					260		
aac	ctc	acc	gtg	gtc	aac	cca	cac	gtt	gat	tcc	acc	ttc	cgc	ttc	atg	931
Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	Thr	Phe	Arg	Phe	Met	
			265					270					275			
aca	ttg	gac	acc	gac	ggc	aag	atc	cgc	atg	gac	tgc	tcc	agc	cca	cac	979
Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	Cys	Ser	Ser	Pro	His	
		280					285					290				
gca	atg	gca	tcg	ctg	att	gac	aac	cga	gac	aag	ttc	gat	gtg	gca	acc	1027
Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	Phe	Asp	Val	Ala	Thr	
	295					300					305					
ggc	aac	gac	gcc	gac	gcc	gac	cgc	cac	ggc	atc	gtc	acc	cca	gac	gct	1075
Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	Val	Thr	Pro	Asp	Ala	
310					315					320					325	
ggc	ttg	atg	aac	ccc	aac	cac	tac	ctc	gca	gta	gca	att	gag	tac	ctc	1123
Gly	Leu	Met	Asn	Pro	Asn	His	Tyr	Leu	Ala	Val	Ala	Ile	Glu	Tyr	Leu	
			330					335					340			
ttt	gct	cac	cgc	cca	ggt	tgg	tcc	gca	gat	acc	gca	gtg	ggc	aaa	acc	1171
Phe	Ala	His		Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	
			345					350					355			
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	gtt	gtg	gcg	cag	ctt	ggc	cgc	1219
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg	
		360					365					370				
acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggt	ttg	1267
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu	
	375					380					385					
atc	tcc	ggc	gaa	atc	gga	ttc	ggt	ggt	gaa	gaa	tcc	gca	ggt	gca	tcc	1315
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser	
390					395				400						405	
ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu	
			410					415					420			
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr	
		425					430					435				
cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggt	gca	cct	gcc	1459
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala	
		440					445					450				
tac	gcc	cgc	acc	gat	gca	gaa	gcc	aac	cga	gaa	caa	aag	gcc	atc	ctg	1507
Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu	
	455					460					465					
aag	gca	ctg	tcc	cca	gaa	cag	gtc	acc	gcc	acc	gaa	cta	gcc	ggc	gaa	1555
Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu	
470					475				480						485	
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile	

	490	495	500	
gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca				1651
Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro				
	505	510	515	
tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc				1699
Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly				
	520	525	530	
gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc				1747
Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser				
	535	540	545	
gaa gta ctc gga cag taaaactgcg gacttgctga caa				1785
Glu Val Leu Gly Gln				
550				

<210> 26

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Met	Ala	His	Glu	Arg	Ala	Gly	Gln	Leu	Ala	Gln	Pro	Glu	Asp	Leu	Ile
1				5					10					15	

Asp	Val	Ala	Glu	Leu	Val	Thr	Ala	Tyr	Phe	Thr	Arg	Lys	Pro	Asp	Val
			20					25					30		

Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly
		35					40					45			

Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr
	50					55					60				

Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly
65				70						75					80

Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met
				85					90					95	

Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val
			100					105					110		

Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile
		115					120					125			

Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg
	130					135					140				

Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg
145					150					155					160

Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr
				165					170					175	

Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly
			180					185					190		

Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu
 195 200 205
 Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
 210 215 220
 Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly
 225 230 235 240
 Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
 245 250 255
 Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
 260 265 270
 Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
 275 280 285
 Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
 290 295 300
 Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
 305 310 315 320
 Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
 325 330 335
 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
 340 345 350
 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
 355 360 365
 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
 370 375 380
 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
 385 390 395 400
 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
 405 410 415
 Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
 420 425 430
 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
 435 440 445
 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
 450 455 460
 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
 465 470 475 480
 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
 485 490 495
 Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
 500 505 510
 Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala

	515					520					525					
Glu	Ser	Phe	Lys	Gly	Glu	Glu	His	Leu	Ala	Gln	Val	Gln	Lys	Glu	Ala	
	530					535					540					
Gln	Ala	Leu	Val	Ser	Glu	Val	Leu	Gly	Gln							
545					550											
 <210> 27																
<211> 680																
<212> DNA																
<213> Corynebacterium glutamicum																
 <220>																
<221> CDS																
<222> (1)..(657)																
<223> RXN02803																
 <400> 27																
gtc	tct	gga	gag	atg	ctc	gcg	gca	gca	ctt	tca	gca	ggc	atg	gcc	agc	48
Val	Ser	Gly	Glu	Met	Leu	Ala	Ala	Ala	Leu	Ser	Ala	Gly	Met	Ala	Ser	
1				5					10					15		
cag	ggt	gtt	gat	gtc	att	cgt	gtt	ggt	gtc	atc	cca	acc	cca	gct	gtt	96
Gln	Gly	Val	Asp	Val	Ile	Arg	Val	Gly	Val	Ile	Pro	Thr	Pro	Ala	Val	
			20					25					30			
gca	ttc	ctc	acc	gat	gat	tat	ggc	gct	gac	atg	ggc	gtg	atg	att	tct	144
Ala	Phe	Leu	Thr	Asp	Asp	Tyr	Gly	Ala	Asp	Met	Gly	Val	Met	Ile	Ser	
		35					40					45				
gca	tcc	cac	aac	cca	atg	ccg	gac	aac	gga	atc	aag	ttc	ttt	tct	gca	192
Ala	Ser	His	Asn	Pro	Met	Pro	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Ser	Ala	
	50					55					60					
ggt	gga	cac	aag	ctt	cca	gac	cat	gtg	gaa	gac	gag	att	gag	cgt	gtt	240
Gly	Gly	His	Lys	Leu	Pro	Asp	His	Val	Glu	Asp	Glu	Ile	Glu	Arg	Val	
65				70						75				80		
atg	gac	agc	ttg	cca	gca	gaa	ggc	cca	aca	ggg	cat	gga	gtt	ggc	cgt	288
Met	Asp	Ser	Leu	Pro	Ala	Glu	Gly	Pro	Thr	Gly	His	Gly	Val	Gly	Arg	
				85					90					95		
gtc	atc	gaa	gaa	gca	acc	gat	gca	cag	gac	cgt	tac	cta	gag	cac	ctg	336
Val	Ile	Glu	Glu	Ala	Thr	Asp	Ala	Gln	Asp	Arg	Tyr	Leu	Glu	His	Leu	
			100					105					110			
aag	gaa	gct	gtt	cct	acg	tca	ctt	gaa	ggc	atc	aag	att	gtt	gtg	gat	384
Lys	Glu	Ala	Val	Pro	Thr	Ser	Leu	Glu	Gly	Ile	Lys	Ile	Val	Val	Asp	
		115					120					125				
gca	gcc	aat	ggt	gcg	gca	agt	gtt	gta	gct	cca	acg	gct	tat	gag	gct	432
Ala	Ala	Asn	Gly	Ala	Ala	Ser	Val	Val	Ala	Pro	Thr	Ala	Tyr	Glu	Ala	
	130					135					140					
gcg	ggt	gca	act	gta	att	gct	att	cat	aac	aag	cca	gac	tca	tac	aac	480
Ala	Gly	Ala	Thr	Val	Ile	Ala	Ile	His	Asn	Lys	Pro	Asp	Ser	Tyr	Asn	
145					150					155					160	
atc	aac	atg	gac	tgc	ggt	tcc	acc	cac	att	gat	cag	gcg	cag	ccg	cca	528

```

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
      165                      170                      175

gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct 576
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
      180                      185                      190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac 624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
      195                      200                      205

caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
      210                      215

gaa 680

<210> 28
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser
  1          5          10          15

Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
      20          25          30

Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
      35          40          45

Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
      50          55          60

Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
      65          70          75          80

Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
      85          90          95

Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
      100         105         110

Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
      115         120         125

Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
      130         135         140

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
      145         150         155         160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
      165                      170                      175

Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
      180                      185                      190

Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp

```


195 200 205

Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
210 215

<210> 29
<211> 399
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(399)
<223> FRXA02803

<400> 29

tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc cag	48
Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln	
1 5 10 15	
ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca	96
Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala	
20 25 30	
ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca	144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala	
35 40 45	
tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt	192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	
50 55 60	
gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg	240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	
65 70 75 80	
gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc	288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	
85 90 95	
atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag	336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	
100 105 110	
gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca	384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala	
115 120 125	
gcc aat ggt gcg gca	399
Ala Asn Gly Ala Ala	
130	

<210> 30
<211> 133
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 30

Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln

42

Gly	Pro	Leu	Arg	Val	Val	Val	Gly	Tyr	Asp	Ala	Arg	Tyr	Gly	Ser	His		
70					75					80					85		
act	ttt	gct	gca	acc	act	gcg	gag	gtg	ttc	gcg	ggg	gct	ggg	ttt	gag	403	
Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	Gly	Ala	Gly	Phe	Glu		
				90					95					100			
gtg	acg	ttg	ctc	ccc	acg	cct	agc	cct	acg	ccg	ttg	att	ccg	tgg	ttg	451	
Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Leu	Ile	Pro	Trp	Leu		
			105					110					115				
gtg	aac	aag	cat	ggg	ttg	gat	gcg	ggc	gtt	cag	atc	acg	gct	tcg	cat	499	
Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	Ile	Thr	Ala	Ser	His		
		120					125					130					
aat	ggg	gcg	gcg	gac	aat	ggc	tac	aag	gtg	ttt	ttg	tct	aat	ggg	cgc	547	
Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg		
	135					140					145						
cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595	
Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala		
150				155				160							165		
gtg	gaa	gat	ccg	att	cgg	gtt	cct	cgg	gtg	acg	gtg	cgc	ccc	act	gct	643	
Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	Val	Arg	Pro	Thr	Ala		
			170					175						180			
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691	
Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	Ser	Leu	Val	Thr	Pro		
			185					190					195				
gat	cag	gct	gat	ttg	ttg	cgg	gtg	aat	tct	gag	cgg	ggc	aat	ctt	cgc	739	
Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg		
		200					205					210					
gtg	gtg	tat	acc	gct	ctg	cat	ggg	gtg	ggg	ggc	cgc	gcg	atg	gcc	aat	787	
Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn		
		215				220					225						
gct	ttc	caa	ttt	gct	ggg	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835	
Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	Gly	Val	Lys	Ala	Gln		
230				235						240				245			
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883	
Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu		
				250					255					260			
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931	
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn		
			265				270						275				
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979	
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val		
		280					285					290					
ggg	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027	
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu		
	295					300					305						
gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggg	gaa	1075	
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu		

310	315	320	325	
ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg				1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu				
	330	335	340	
ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg				1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr				
	345	350	355	
gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt				1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu				
	360	365	370	
gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc				1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val				
	375	380	385	
gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg				1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp				
	390	395	400	405
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat				1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn				
	410	415	420	
gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg				1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val				
	425	430	435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct				1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro				
	440	445	450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa				1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu				
	455	460	465	
aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt				1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg				
	470	475	480	485
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg				1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu				
	490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat				1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His				
	505	510	515	
cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg				1700
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser Lys Leu				
	520	525	530	
gctgctcccg gtt				1713

<210> 32

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
 1 5 10 15
 Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
 20 25 30
 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240
 Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320

Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	
				325					330							
Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	
				340					345							
Ser	Glu	Thr	Leu	Thr	Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	
				355					360							
Leu	Asp	Gly	Pro	Leu	Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	
				370					375							
Pro	Val	Pro	Asp	Val	Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	
				385					390							
Phe	Met	Ala	Ser	Trp	Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	
				405					410							
Gln	Gln	Lys	Leu	Asn	Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser	
				420					425							
Ser	Gln	Ile	Ala	Val	Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	
				435					440							
Trp	Ile	Ala	His	Pro	Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	
				450					455							
His	Ile	Leu	Pro	Glu	Lys	Gln	Gly	Ile	Ala	Leu	His	Gly	Gln	Val	Gly	
				465					470							
His	Val	His	Ile	Arg	Ala	Ile	Gly	Arg	Val	Ser	Gly	Thr	Glu	Ala	Lys	
				485					490							
Ala	Lys	Leu	Tyr	Leu	Glu	Val	Gly	Gln	Ala	Ser	Ser	His	Asp	Glu	Ala	
				500					505							
Ala	Gln	Leu	Leu	His	Gln	Leu	Glu	Asp	Glu	Val	Gln	Ser	Trp	Leu	Ser	
				515					520							
Lys	Leu															
				530												

```
<210> 33
<211> 1684
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1684)
<223> FRXA02854
```

<400> 33
aataccttttc tgttttqtcc qcagqcgat caqqaiaacc tqcagcgcgg tagagtcgag 60

tctaatagtg atccccagaa aacaaaggat cggggtgttc atg gac gag tct cgt 115
Met Asp Glu Ser Arg
1 5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg	163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala	
10 15 20	
cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt	211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val	
25 30 35	
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg	259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu	
40 45 50	
gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat	307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp	
55 60 65	
ggg ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat	355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His	
70 75 80 85	
act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag	403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu	
90 95 100	
gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg	451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu	
105 110 115	
gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat	499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His	
120 125 130	
aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt gcg	547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg	
135 140 145	
cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct	595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala	
150 155 160 165	
gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct	643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala	
170 175 180	
gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct	691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro	
185 190 195	
gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc	739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg	
200 205 210	
gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat	787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn	
215 220 225	
gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag	835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln	
230 235 240 245	
cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa	883

Gln Tyr Pro Asp	Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu	
	250 255 260	
gag cct tct gcg att gag ttg ttg ttg gaa cgc gca aag gaa aag aac	931	
Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn		
	265 270 275	
gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg	979	
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val		
	280 285 290	
ggt att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag	1027	
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu		
	295 300 305	
gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa	1075	
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu		
	310 315 320 325	
ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg	1123	
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu		
	330 335 340	
ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg	1171	
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr		
	345 350 355	
gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt	1219	
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu		
	360 365 370	
gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc	1267	
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val		
	375 380 385	
gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg	1315	
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp		
	390 395 400 405	
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat	1363	
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn		
	410 415 420	
gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg	1411	
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val		
	425 430 435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct	1459	
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro		
	440 445 450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa	1507	
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu		
	455 460 465	
aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt	1555	
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg		
	470 475 480 485	
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg	1603	
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu		

490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat			1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His			
505	510	515	
cag ctg gag gat gaa gtc caa agc tgg ttg agc			1684
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser			
520	525		
<210> 34			
<211> 528			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 34			
Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala			
1	5	10	15
Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg			
20	25	30	
Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn			
35	40	45	
Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala			
50	55	60	
Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala			
65	70	75	80
Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala			
85	90	95	
Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro			
100	105	110	
Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln			
115	120	125	
Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe			
130	135	140	
Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu			
145	150	155	160
Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr			
165	170	175	
Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val			
180	185	190	
Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu			
195	200	205	
Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly			
210	215	220	
Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His			
225	230	235	240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320
 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
 500 505 510
 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
 515 520 525

<210> 35

<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00511

<400> 35

gag	ctg	cgc	aag	aac	acc	ctc	gtg	ggc	act	gtc	atg	agc	aac	ctg	gga	48
Glu	Leu	Arg	Lys	Asn	Thr	Leu	Val	Gly	Thr	Val	Met	Ser	Asn	Leu	Gly	
1				5					10					15		

ttg	aag	att	gct	atg	gat	gaa	gcc	gga	att	aca	ctg	cgt	acc	acc	aag	96
Leu	Lys	Ile	Ala	Met	Asp	Glu	Ala	Gly	Ile	Thr	Leu	Arg	Thr	Thr	Lys	
			20					25					30			

gta	gga	gac	cgc	tac	gtg	ctg	gaa	gac	ctc	aat	gca	ggt	gga	ttc	agc	144
Val	Gly	Asp	Arg	Tyr	Val	Leu	Glu	Asp	Leu	Asn	Ala	Gly	Gly	Phe	Ser	
		35					40					45				

ctg	ggc	ggc	gag	caa	tct	ggc	cac	att	gtt	ctt	cca	gat	cat	ggc	acc	192
Leu	Gly	Gly	Glu	Gln	Ser	Gly	His	Ile	Val	Leu	Pro	Asp	His	Gly	Thr	
	50					55					60					

act	ggc	gat	gga	act	ttg	act	ggt	ctt	tcc	atc	atg	gcg	cgc	atg	gct	240
Thr	Gly	Asp	Gly	Thr	Leu	Thr	Gly	Leu	Ser	Ile	Met	Ala	Arg	Met	Ala	
65					70					75					80	

gaa	acc	gga	aag	tcc	ttg	ggc	gag	ttg	gca	caa	gct	atg	acg	gtg	ctg	288
Glu	Thr	Gly	Lys	Ser	Leu	Gly	Glu	Leu	Ala	Gln	Ala	Met	Thr	Val	Leu	
				85					90					95		

cca	cag	gtt	ctg	atc	aat	gtg	cca	gtt	tcg	gat	aag	tcc	acc	atc	gtg	336
Pro	Gln	Val	Leu	Ile	Asn	Val	Pro	Val	Ser	Asp	Lys	Ser	Thr	Ile	Val	
			100					105					110			

agc	cac	cca	agc	gtt	gtg	gct	gcg	atc	gcg	gaa	gca	gaa	gct	gag	ttg	384
Ser	His	Pro	Ser	Val	Val	Ala	Ala	Ile	Ala	Glu	Ala	Glu	Ala	Glu	Leu	
		115				120					125					

ggc	gcc	acc	ggt	cgc	gtt	ctt	ctt	cgt	gct	tct	ggc	acc	gaa	gag	ctt	432
Gly	Ala	Thr	Gly	Arg	Val	Leu	Leu	Arg	Ala	Ser	Gly	Thr	Glu	Glu	Leu	
	130					135					140					

ttc	cgc	gtg	atg	gtt	gag	gct	gga	gac	aag	gaa	caa	gct	cgt	cgt	atc	480
Phe	Arg	Val	Met	Val	Glu	Ala	Gly	Asp	Lys	Glu	Gln	Ala	Arg	Arg	Ile	
145					150					155					160	

gcg	gga	cgt	ctt	gct	gca	gtg	gtt	gca	gaa	gtc	taattcactt	cagtcacagc	533
Ala	Gly	Arg	Leu	Ala	Ala	Val	Val	Ala	Glu	Val			
				165				170					

gca																536
-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	-----

<210> 36

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Glu Leu Arg Lys Asn Thr Leu Val Gly Thr Val Met Ser Asn Leu Gly
 1 5 10 15
 Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
 20 25 30
 Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45
 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80
 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
 130 135 140
 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
 145 150 155 160
 Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
 165 170

<210> 37

<211> 1497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN01365

<400> 37

cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60
 ttgcaagcgt tattttgttc cctaaccctc tcgaggattt atg cgt acc cgt gaa 115
 Met Arg Thr Arg Glu
 1 5
 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35
 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val	Ala	Ile	Gly	His	Asp		
		40					45					50					
atg	cgt	gat	tcc	tcc	cct	gaa	ttg	gcc	aag	gcg	ttt	gcc	gat	ggc	gtg	307	
Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala	Phe	Ala	Asp	Gly	Val		
		55				60				65							
act	gca	cag	ggt	ttg	gat	gtt	gtt	cat	ttg	gga	ctg	act	tct	act	gat	355	
Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly	Leu	Thr	Ser	Thr	Asp		
		70			75					80					85		
gag	ctg	tac	ttt	gcg	tcc	gga	acc	ttg	aag	tgt	gct	ggt	gcg	atg	ttt	403	
Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys	Ala	Gly	Ala	Met	Phe		
				90					95					100			
act	gcg	tcg	cat	aac	ccc	gct	gag	tac	aac	ggc	atc	aag	ttg	tgt	cgt	451	
Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggt	gct	cgt	ccg	gtc	ggt	cag	gat	tct	ggt	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
		120					125					130					
gat	gat	ctg	gtt	gag	ggt	gtt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
		135				140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
		150			155					160					165		
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170					175					180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
		200					205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
		215				220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
		230			235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250					255					260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		

280	285	290	
gag gtg att gct gaa aac ggt ggc act gcg gtg cgt act cgc gtg ggt			1027
Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val Arg Thr Arg Val Gly			
295	300	305	
cac tcc ttc atc aag gcg aag atg gca gag acc ggt gcg gcc ttt ggt			1075
His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr Gly Ala Ala Phe Gly			
310	315	320	325
ggc gag cac tct gcg cac tac tac ttc act gag ttc ttc aat gcg gac			1123
Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu Phe Phe Asn Ala Asp			
	330	335	340
tcc ggc att ttg gct gcg atg cac gtg ctg gct gcg ctg gga agc cag			1171
Ser Gly Ile Leu Ala Ala Met His Val Leu Ala Ala Leu Gly Ser Gln			
	345	350	355
gac cag cca ctc agt gag atg atg gct agg tat aac cgg tac gtt gct			1219
Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr Asn Arg Tyr Val Ala			
	360	365	370
tca ggc gag ttg aac tcc cgt ttg gct aat gca gag gcg cag caa gag			1267
Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala Glu Ala Gln Gln Glu			
	375	380	385
cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg			1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val			
	395	400	405
gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg			1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp			
	410	415	420
ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt			1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val			
	425	430	435
gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta			1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu			
	440	445	450
ggg att atc cgc gca taatcccatt ttccggcggg cat			1497
Gly Ile Ile Arg Ala			
455			

<210> 38

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

Met	Arg	Thr	Arg	Glu	Ser	Val	Thr	Ala	Val	Ile	Lys	Ala	Tyr	Asp	Val
1				5					10					15	

Arg	Gly	Val	Val	Gly	Val	Asp	Ile	Asp	Ala	Asp	Phe	Ile	Ser	Glu	Thr
		20						25					30		

Gly	Ala	Ala	Phe	Gly	Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val
	35						40					45			

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
 290 295 300
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
 305 310 315 320
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
 325 330 335
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
 340 345 350
 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
 355 360 365

Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
 420 425 430
 Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu
 435 440 445
 Val Ala Glu Ile Leu Gly Ile Ile Arg Ala
 450 455

<210> 39
 <211> 994
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(994)
 <223> FRXA01365

<400> 39
 cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60
 ttgcaagcgt tattttgttc cctaaccctt tcgaggattt atg cgt acc cgt gaa 115
 Met Arg Thr Arg Glu
 1 5
 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35
 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
 40 45 50
 atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
 55 60 65
 act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
 70 75 80 85
 gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
 Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
 90 95 100
 act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451

Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggt	gct	cgt	ccg	gtc	ggt	cag	gat	tct	ggt	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
			120				125					130					
gat	gat	ctg	gtt	gag	ggt	gtt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
			135			140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
150					155					160					165		
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170				175						180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
			200				205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
			215			220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
230					235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250				255						260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		
			280				285					290					
gag	gtg	att	gct	gaa												994	
Glu	Val	Ile	Ala	Glu													
				295													

<210> 40

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

Met	Arg	Thr	Arg	Glu	Ser	Val	Thr	Ala	Val	Ile	Lys	Ala	Tyr	Asp	Val
1				5					10					15	

Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
 20 25 30
 Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45
 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
 290 295

<210> 41

<211> 1743

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1720)

<223> RXA00098

<400> 41

```

taaattgtc gtgtttccca ctttgaacac tcttcgatgc gcttggccac aaaagcaagc 60

taacctgaag atgttattta acgacaataa aggagttttc atg gcg gac att tcg 115
                                         Met Ala Asp Ile Ser
                                         1 5

acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
                        10 15 20

gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
                        25 30 35

tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
                        40 45 50

ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307
Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser
                        55 60 65

ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac ctc aac 355
Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn
                        70 75 80 85

aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt cct gcc 403
Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala
                        90 95 100

gaa gct gat ctg tca gta gat ggc caa gat gtt gct gct gat gtc cac 451
Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His
                        105 110 115

gaa gtt ttg gga cgc atg cgt gac ttc gct act gcg ctg cgc tca ggc 499
Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly
                        120 125 130

aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc aac att 547
Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile
                        135 140 145

ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag gct ctg 595
Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu
                        150 155 160 165

cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc aac gtc 643
Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val
                        170 175 180

gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc 691
Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser
                        185 190 195

aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag acg ctg 739
Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu

```

200	205	210	
tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc ggt gaa			787
Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu			
215	220	225	
gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct gaa aag			835
Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys			
230	235	240	245
gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc tgg gac			883
Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp			
250	255	260	
tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt tcc ctc			931
Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu			
265	270	275	
atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt gga ttc			979
Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe			
280	285	290	
cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag aac gtt			1027
His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val			
295	300	305	
cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt			1075
Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly			
310	315	320	325
gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt			1123
Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe			
330	335	340	
gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc			1171
Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val			
345	350	355	
cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg			1219
His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp			
360	365	370	
ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac			1267
Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His			
375	380	385	
cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca			1315
Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro			
390	395	400	405
aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg			1363
Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met			
410	415	420	
agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct			1411
Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala			
425	430	435	
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag			1459
Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys			
440	445	450	

gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt 1507
 Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
 455 460 465

acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
 Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
 470 475 480 485

atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt 1603
 Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
 490 495 500

gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct 1651
 Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
 505 510 515

ggg gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att 1699
 Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
 520 525 530

aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag 1743
 Lys Trp Tyr Arg Ala Asn Arg
 535 540

<210> 42

<211> 540

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met Ala Asp Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His
 1 5 10 15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
 35 40 45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
 165 170 175
 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
 180 185 190
 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
 195 200 205
 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
 210 215 220
 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
 225 230 235 240
 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
 245 250 255
 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
 260 265 270
 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
 275 280 285
 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
 290 295 300
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
 305 310 315 320
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
 325 330 335
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
 340 345 350
 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
 355 360 365
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
 405 410 415
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
 420 425 430
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
 435 440 445
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
 450 455 460
 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
 465 470 475 480

Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
 500 505 510

Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
 515 520 525

Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
 530 535 540

<210> 43
 <211> 630
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(630)
 <223> RXA01989

<400> 43
 gtt aaa tca att cac aaa aca att cat gaa ggt act ggt gca ggt agt 48
 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
 1 5 10 15

gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa 96
 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat 144
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca 192
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct 240
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag 288
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct 336
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa 384
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata 432
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca 480

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga 528
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga 576
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190
 att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa 624
 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205
 tta tct 630
 Leu Ser
 210

<210> 44
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
 1 5 10 15
 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140
 Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
 210

<210> 45

<211> 1269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXA00340

<400> 45

cggatctctcc gacatccgca acacccccaa agatgaggtt ccacagtgcc cagaatgtgg 60

ctcttacctc atcactgaca tctcttagaa agaccaccca gtg aaa tta gtc atc 115
 Val Lys Leu Val Ile
 1 5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc 163
 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
 10 15 20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc 211
 Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
 25 30 35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga 259
 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
 40 45 50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg 307
 Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
 55 60 65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355
 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
 70 75 80 85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403
 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
 90 95 100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451
 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
 105 110 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499
 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
 120 125 130

gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta 547
 Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
 135 140 145

tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc	595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
150 155 160 165	
acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	
gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc	883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
250 255 260	
gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg	1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
310 315 320 325	
gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
330 335 340	
gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg	1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg	1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
360 365 370	
ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag	1266
Phe Asn Asp Thr Ser His Leu Glu Ala	
375 380	
ctc	1269

<210> 46

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly
 1 5 10 15

Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val
 20 25 30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
 35 40 45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
 50 55 60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65 70 75 80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
 85 90 95

Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
 100 105 110

Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
 115 120 125

Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
 130 135 140

Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
 145 150 155 160

Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
 165 170 175

Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
 180 185 190

Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
 195 200 205

Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
 210 215 220

Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
 225 230 235 240

Gln Thr Ala Glu Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
 245 250 255

Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser
 260 265 270

Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
 275 280 285

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
 290 295 300
 Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
 305 310 315 320
 Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
 325 330 335
 Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
 340 345 350
 Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
 355 360 365
 Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala
 370 375 380

<210> 47
 <211> 840
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(817)
 <223> RXA02492

<400> 47
 gctgtacaac gacgctattg ccaacgaaaa tgtcgacggt gaaacgcac acggctaagt 60
 aaacgcgcgt cgtggaacat aaagtggcaa actagtagcct atg act aac gga aaa 115
 Met Thr Asn Gly Lys
 1 5
 ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
 Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
 10 15 20
 ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
 Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
 25 30 35
 gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
 Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
 40 45 50
 gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
 Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
 55 60 65
 atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
 Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
 70 75 80 85
 ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
 Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
 90 95 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
 Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
 105 110 115
 gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
 Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
 120 125 130
 ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
 Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
 135 140 145
 ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
 Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
 150 155 160 165
 gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
 Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
 170 175 180
 aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
 Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
 185 190 195
 cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
 200 205 210
 gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
 215 220 225
 gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837
 Ala Ala Val Ala Asn Gln Gly Asn Lys
 230 235
 ctc 840

<210> 48

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
 1 5 10 15
 Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
 20 25 30
 Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
 35 40 45
 Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
 50 55 60
 Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65 70 75 80
 Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu

70

55	60	65	
aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca			355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala			
70	75	80	85
ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg			403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu			
	90	95	100
tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc			451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser			
	105	110	115
tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg			499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val			
	120	125	130
gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc			547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr			
	135	140	145
cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc			595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser			
	150	155	160
ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca			643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr			
	170	175	180
tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa			691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu			
	185	190	195
cca gct cag gag att tgatcactcg tgcgtttgac caa			729
Pro Ala Gln Glu Ile			
	200		

<210> 50

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
1 5 10 15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
20 25 30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
35 40 45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
50 55 60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
65 70 75 80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly

tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc 355
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser
70 75 80 85

gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat 403
 Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
 90 95 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag 451
 Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
 105 110 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt 499
 Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
 120 125 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc 547
 Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
 135 140 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat 595
 Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
 150 155 160 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg 643
 Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
 170 175 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
 230

<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
 1 5 10 15

Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
 20 25 30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
 50 55 60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

Ala	Pro	Thr	Val	Ser 85	Ala	His	Gly	Leu	Glu 90	Leu	Thr	Val	Glu	Pro 95	Gly
Leu	Ile	Glu	Cys 100	Asp	Phe	Gly	Glu	Trp 105	Thr	Gly	Arg	Lys	Leu 110	Thr	Glu
Leu	Asn	Ala 115	Leu	Glu	Glu	Trp	Lys 120	Ala	Val	Gln	Lys	Thr 125	Pro	Ser	Thr
Phe	Arg 130	Phe	Pro	Gly	Gly	Glu	Ser 135	Phe	Val	Glu	Met 140	Gln	Asp	Arg	Met
Val 145	Glu	Ala	Ile	Gly	Asn 150	Ile	Ala	Gln	Gln 155	His	Pro	Gly	Glu	Ile	Val 160
Ala	Ala	Phe	Ser	His 165	Ala	Asp	Thr	Ile	Lys 170	Ala	Ala	Val	Ala	His 175	Phe
Val	Gly	Thr	Pro 180	Leu	Asp	Ser	Phe	Gln 185	Arg	Ile	Phe	Ile	Asp 190	Thr	Ala
Ser	Ile 195	Ser	Ala	Val	Glu	Phe	Thr 200	Gly	Lys	Ser	Ser	Gly 205	Val	Ser	Ser
His 210	Met	Leu	Leu	Thr	Asn 215	Ser	Arg	Thr	Gly	Ser	Leu 220	Gly	Tyr	Leu	Arg
Asp 225	Lys	Leu	Pro	Lys 230	Ala	Pro	Gln	Pro							

```
<210> 53
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1138)
<223> RXA00206
```

```

<400> 53
ttaaataaga tggtcagaga cagttttttg gcctgtcaac ccctgtgatt ctcttatttt 60

tgggtgattg ttccggcgcg ggtgttgatga tgggtttaat atg gaa gac atg cga 115
Met Glu Asp Met Arg
1 5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
10 15 20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
25 30 35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
40 45 50

```

cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc	307
Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly	
55 60 65	
acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga	355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly	
70 75 80 85	
att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt	403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu	
90 95 100	
atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct	451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser	
105 110 115	
gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac	499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp	
120 125 130	
gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg	547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val	
135 140 145	
gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac	595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn	
150 155 160 165	
cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct	643
Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala	
170 175 180	
ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa	691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu	
185 190 195	
gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc	739
Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe	
200 205 210	
cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg	787
Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu	
215 220 225	
cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc	835
Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe	
230 235 240 245	
ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc	883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile	
250 255 260	
cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att	931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile	
265 270 275	
caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt	979
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg	
280 285 290	
tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag	1027

Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305
 gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
 310 315 320 325
 gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
 330 335 340
 cag gca atg ttt gga tagtttttctg ggcttttatc aac 1161
 Gln Ala Met Phe Gly
 345

<210> 54

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
 1 5 10 15
 Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
 20 25 30
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
 35 40 45
 Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60
 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80
 Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95
 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110
 Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125
 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140
 Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
 145 150 155 160
 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190
 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
 305 310 315 320

Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
 325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
 340 345

<210> 55
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXA01243

<400> 55
 gcgcaatcag cgatatcgat gtggtggtca ccgatgcggg tgcaccagca agtttcggtg 60
 agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115
 Met Ile Leu Thr Val
 1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
 10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
 25 30 35

ggg ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
 40 45 50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
 55 60 65

gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc	355
Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro	
70 75 80 85	
atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag	403
Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys	
90 95 100	
ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt	451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu	
105 110 115	
cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg	499
Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu	
120 125 130	
ggg ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg	547
Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val	
135 140 145	
gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca	595
Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala	
150 155 160 165	
gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg	643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr	
170 175 180	
tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act	691
Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr	
185 190 195	
gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc	739
Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu	
200 205 210	
tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc	787
Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr	
215 220 225	
gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag	835
Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu	
230 235 240 245	
tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc	883
Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly	
250 255 260	
gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat	931
Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn	
265 270 275	
gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc	979
Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala	
280 285 290	
aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag	1027
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys	
295 300 305	
ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc	1080

Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
 310 315 320

aaa

1083

<210> 56

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu
 1 5 10 15

Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val
 20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe
 35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
 50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
 65 70 75 80

Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
 85 90 95

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
 100 105 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
 115 120 125

Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
 130 135 140

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
 145 150 155 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
 165 170 175

Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
 180 185 190

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
 195 200 205

Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
 210 215 220

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
 225 230 235 240

Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
 245 250 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

	260		265		270										
Leu	Ala	Ala	Ser	Asn	Asp	Gly	Lys	Ser	Thr	Glu	Asp	Ser	Val	Ile	Asn
	275					280					285				
Ala	Val	Ala	Tyr	Ala	Asn	Ala	Glu	Gly	Ser	Glu	Trp	Asp	Asn	Tyr	Ile
	290				295					300					
Pro	Thr	Pro	Asp	Lys	Leu	Arg	Ala	Glu	His	Val	Val	Ile	Lys	Ser	Leu
305					310					315					320

<210> 57
 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXA01882

<400> 57
 accctttttc caccttggtt gattttgatg cccttggtac cgatgaccac acgctagatt 60

ttccagtttt gcccgaccac aactttcagg tggttaacccc atg atc atc aca ttc 115
 Met Ile Ile Thr Phe
 1 5

acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc 163
 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
 10 15 20

tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211
 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
 25 30 35

ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50

acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65

gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85

gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
 90 95 100

ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
 Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
 105 110 115

gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc 499

Glu	Lys	Val	Leu	Ile	Asp	Ala	Leu	Arg	Pro	Glu	Val	Thr	Trp	Val	Val		
		120					125					130					
ctg	gcg	ggc	tcg	ctg	cca	cca	ggg	gca	cca	gtt	gac	tggtac	gcg	cgt		547	
Leu	Ala	Gly	Ser	Leu	Pro	Pro	Gly	Ala	Pro	Val	Asp	Trp	Tyr	Ala	Arg		
		135					140					145					
ctc	acc	gcg	ttg	atc	cat	tca	gca	cgc	cct	gac	gtt	cgc	gtg	gct	gtc	595	
Leu	Thr	Ala	Leu	Ile	His	Ser	Ala	Arg	Pro	Asp	Val	Arg	Val	Ala	Val		
					155					160					165		
gat	acc	tca	gac	aag	cca	ctg	atg	gcg	ttg	ggc	gag	agc	ttg	gat	aca	643	
Asp	Thr	Ser	Asp	Lys	Pro	Leu	Met	Ala	Leu	Gly	Glu	Ser	Leu	Asp	Thr		
				170					175					180			
cct	ggc	gct	gct	ccg	aac	ctg	att	aag	cca	aat	ggg	ctg	gaa	ctg	ggc	691	
Pro	Gly	Ala	Ala	Pro	Asn	Leu	Ile	Lys	Pro	Asn	Gly	Leu	Glu	Leu	Gly		
				185				190					195				
cag	ctg	gct	aac	act	gat	ggg	gaa	gag	ctg	gag	gag	cgt	gct	gag	caa	739	
Gln	Leu	Ala	Asn	Thr	Asp	Gly	Glu	Glu	Leu	Glu	Ala	Arg	Ala	Ala	Gln		
			200				205					210					
ggc	gat	tac	gac	gcc	atc	atc	gca	gct	gag	gac	gta	ctg	gtt	aac	cgt	787	
Gly	Asp	Tyr	Asp	Ala	Ile	Ile	Ala	Ala	Ala	Asp	Val	Leu	Val	Asn	Arg		
					220						225						
ggc	atc	gaa	cag	gtg	ctt	gtc	acc	ttg	ggg	gcc	gca	gga	gag	gtg	ttg	835	
Gly	Ile	Glu	Gln	Val	Leu	Val	Thr	Leu	Gly	Ala	Ala	Gly	Ala	Val	Leu		
					235				240						245		
gtc	aac	gca	gaa	ggg	gag	tggt	act	gct	act	tct	cca	aag	att	gat	gtt	883	
Val	Asn	Ala	Glu	Gly	Ala	Trp	Thr	Ala	Thr	Ser	Pro	Lys	Ile	Asp	Val		
				250					255					260			
gta	tcc	acc	gtt	gga	gct	gga	gac	tgt	gct	ctt	gca	ggg	ttt	gtt	atg	931	
Val	Ser	Thr	Val	Gly	Ala	Gly	Asp	Cys	Ala	Leu	Ala	Gly	Phe	Val	Met		
				265				270						275			
gca	cgt	tcc	cag	aag	aaa	aca	ctg	gag	gaa	tct	ctg	ctg	aat	gcc	gtg	979	
Ala	Arg	Ser	Gln	Lys	Lys	Thr	Leu	Glu	Glu	Ser	Leu	Leu	Asn	Ala	Val		
				280			285						290				
tct	tac	ggc	tcg	act	gag	gag	tct	ctt	cct	ggc	act	acc	att	cct	cgt	1027	
Ser	Tyr	Gly	Ser	Thr	Ala	Ala	Ser	Leu	Pro	Gly	Thr	Thr	Ile	Pro	Arg		
					300												
cct	gac	caa	ctc	gcc	aca	gct	ggg	gca	acg	gtc	acc	caa	gtc	aaa	gga	1075	
Pro	Asp	Gln	Leu	Ala	Thr	Ala	Gly	Ala	Thr	Val	Thr	Gln	Val	Lys	Gly		
					315					320					325		
ttg	aaa	gaa	tca	gca	tgaatagcgt	aaataattcc	tcg									1113	
Leu	Lys	Glu	Ser	Ala													
				330													

<210> 58

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser
 1 5 10 15
 Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val
 20 25 30
 Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
 35 40 45
 Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
 50 55 60
 Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65 70 75 80
 Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
 85 90 95
 Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
 100 105 110
 Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
 115 120 125
 Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
 130 135 140
 Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
 145 150 155 160
 Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
 165 170 175
 Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
 180 185 190
 Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
 195 200 205
 Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
 210 215 220
 Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
 225 230 235 240
 Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
 245 250 255
 Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
 260 265 270
 Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
 275 280 285
 Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
 290 295 300
 Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
 305 310 315 320

Thr Gln Val Lys Gly Leu Lys Glu Ser Ala
 325 330

<210> 59
 <211> 1155
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1132)
 <223> RXA01702

<400> 59
 attgtgaatg tgggattatc ggttcgcgct tcaccatggt tctgcatgat gaaattacat 60

acatagttca gtgacagtca ccttttggag gagacacctt atg cct atc gca act 115
 Met Pro Ile Ala Thr
 1 5

ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163
 Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
 10 15 20

gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct 211
 Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
 25 30 35

ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc 259
 Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
 40 45 50

acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc 307
 Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
 55 60 65

aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc 355
 Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
 70 75 80 85

tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc 403
 Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
 90 95 100

ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc 451
 Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
 105 110 115

gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc 499
 Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
 120 125 130

gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct 547
 Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
 135 140 145

aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc 595
 Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
 150 155 160 165

ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac 643
 Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
 170 175 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt 691
 Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
 185 190 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc 739
 Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
 200 205 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag 787
 Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
 215 220 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt 835
 Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
 230 235 240 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag 883
 Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
 250 255 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
 310 315 320 325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
 Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
 330 335 340

acc tct aag taatctcagc agttaaaaag ggc 1155
 Thr Ser Lys

<210> 60

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Pro Ile Ala Thr Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala
 1 5 10 15

Lys Glu Gly Gly Phe Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
 20 25 30

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
 50 55 60
 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
 85 90 95
 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
 100 105 110
 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160
 Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
 290 295 300
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
 305 310 315 320
 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
 325 330 335
 Ser Val Gly Lys Thr Thr Ser Lys
 340

```
<210> 61
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(877)  
<223> RXA02258
```

<400> 61																
cggttgcaatt	ctcgcctcagt	aaatccgaca	cggccctttg	ttagaaaaca	aaacataaag	60										
ggccaccggg	aaactttttt	aagaaagggtg	tgtttcacac	atg	gca	cgt	aag	cca								115
				Met	Ala	Arg	Lys	Pro								5
				1												
ctt	atc	gct	ggg	aac	tgg	aag	atg	aac	ctg	gat	cac	cag	cag	gca	atc	163
Leu	Ile	Ala	Gly	Asn	Trp	Lys	Met	Asn	Leu	Asp	His	Gln	Gln	Ala	Ile	
			10					15							20	
ggc	act	gtt	cag	aag	ctt	gca	ttc	gcc	ctt	cca	aag	gaa	tac	ttc	gag	211
Gly	Thr	Val	Gln	Lys	Leu	Ala	Phe	Ala	Leu	Pro	Lys	Glu	Tyr	Phe	Glu	
			25					30							35	
aag	gtt	gac	gtt	gca	gtc	acc	gtt	cct	ttc	act	gac	atc	cgc	tcc	gtc	259
Lys	Val	Asp	Val	Ala	Val	Thr	Val	Pro	Phe	Thr	Asp	Ile	Arg	Ser	Val	
		40					45							50		
cag	act	ctc	gtt	gag	ggc	gac	aag	ctt	gag	gtc	act	ttc	ggg	gct	cag	307
Gln	Thr	Leu	Val	Glu	Gly	Asp	Lys	Leu	Glu	Val	Thr	Phe	Gly	Ala	Gln	
		55					60							65		
gac	gtc	tcc	cag	cac	gag	tcc	ggg	gcg	tac	acc	ggg	gaa	gtt	tct	gca	355
Asp	Val	Ser	Gln	His	Glu	Ser	Gly	Ala	Tyr	Thr	Gly	Glu	Val	Ser	Ala	
70					75							80			85	
agc	atg	ctg	gca	aag	ttg	aac	tgc	tct	tgg	gtt	gtc	gtt	gga	cac	tcc	403
Ser	Met	Leu	Ala	Lys	Leu	Asn	Cys	Ser	Trp	Val	Val	Val	Gly	His	Ser	
			90					95							100	
gag	cgc	cgc	gag	tac	cac	aac	gag	tct	gat	gag	ttg	gtt	gct	gcg	aag	451
Glu	Arg	Arg	Glu	Tyr	His	Asn	Glu	Ser	Asp	Glu	Leu	Val	Ala	Ala	Lys	
			105					110							115	
gca	aag	gca	gct	ctg	tcc	aac	ggc	atc	agc	ccg	atc	gtc	tgc	gtt	ggg	499
Ala	Lys	Ala	Ala	Leu	Ser	Asn	Gly	Ile	Ser	Pro	Ile	Val	Cys	Val	Gly	
		120					125							130		
gag	cca	ctg	gaa	atc	cgt	gaa	gct	ggc	acc	cac	gtt	gag	tac	gtc	gtc	547
Glu	Pro	Leu	Glu	Ile	Arg	Glu	Ala	Gly	Thr	His	Val	Glu	Tyr	Val	Val	
		135					140							145		
gag	cag	acc	cgt	aag	tcc	ctt	gct	ggc	ctg	gat	gct	gct	gag	ctg	gcc	595
Glu	Gln	Thr	Arg	Lys	Ser	Leu	Ala	Gly	Leu	Asp	Ala	Ala	Glu	Leu	Ala	
150					155							160			165	
aac	acc	gtt	atc	gcg	tat	gag	cca	gtg	tgg	gct	atc	ggc	acc	ggg	aag	643
Asn	Thr	Val	Ile	Ala	Tyr	Glu	Pro	Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	
			170					175							180	

```

gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt 691
Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
      185                      190                      195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att 739
Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
      200                      205                      210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
      215                      220                      225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
      230                      235                      240                      245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala
      250                      255

taaagtacag agctttaag cac 900

```

<210> 62
 <211> 259
 <212> PRT
 <213> *Corynebacterium glutamicum*

```

<400> 62
Met Ala Arg Lys Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
  1              5              10              15

His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro
      20              25              30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
      35              40              45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
      50              55              60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
      65              70              75              80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
      85              90              95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
      100             105             110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
      115             120             125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
      130             135             140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
      145             150             155             160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
      165             170             175

```

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
 210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
 225 230 235 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
 245 250 255

Ser Val Ala

<210> 63
 <211> 1563
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1540)
 <223> RXN01225

<400> 63
 tttgggctaa tggtgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccggttaaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa	451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu	
105 110 115	
acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
120 125 130	
ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac	547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
215 220 225	
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag	835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
250 255 260	
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
280 285 290	
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa	1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171

Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
 345 350 355

aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg 1219
 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370

gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385

aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405

atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420

acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435

cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480

cac 1563

<210> 64

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
 1 5 10 15

Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
 20 25 30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110
 Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
 435 440 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
 450 455 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 465 470 475 480

<210> 65
 <211> 1563
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1540)
 <223> FRXA01225

<400> 65
 tttgggctaa tggtgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccgggttaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
 Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
 105 110 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
120 125 130	
ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac	547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
215 220 225	
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag	835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
250 255 260	
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
280 285 290	
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa	1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly	
345 350 355	
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg	1219

Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
 gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480
 cac 1563

<210> 66

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
 1 5 10 15
 Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
 20 25 30
 Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95
 Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415
 Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430
 Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn

96


```

ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc 547
Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser
135 140 145

ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta 595
Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu
150 155 160 165

aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca 643
Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala
170 175 180

tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt 691
Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg
185 190 195

cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca 739
Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala
200 205 210

gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac 787
Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp
215 220 225

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg 835
Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
230 235 240 245

acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca 883
Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
250 255 260

atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc 931
Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
265 270 275

gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc 979
Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
280 285 290

atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt 1027
Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
295 300 305

gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt 1075
Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
310 315 320 325

ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa 1122
Leu Thr Glu Leu Val Ala Ser Lys Leu
330

cgt 1125

```

<210> 68

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
 1 5 10 15
 Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
 20 25 30
 Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
 35 40 45
 Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
 50 55 60
 Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
 65 70 75 80
 Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
 85 90 95
 Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
 100 105 110
 Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
 115 120 125
 Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
 130 135 140
 His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
 145 150 155 160
 Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
 165 170 175
 Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
 180 185 190
 His Arg Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
 195 200 205
 Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 210 215 220
 Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
 225 230 235 240
 Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
 245 250 255
 Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
 260 265 270
 Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
 275 280 285
 Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
 290 295 300
 Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
 305 310 315 320
 Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu

325

330

```
<210> 69
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1315)
<223> RXA02257
```

<400> 69																
ataccggtgc cagcgccaca caatgtgtgg caatctggga cagtgcaccca cattgcacca 60																
gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc 115																
Met Ala Val Lys Thr 5																
ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163																
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val 20																
cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat 211																
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp 35																
aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa 259																
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu 50																
ggg ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc 307																
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly 65																
gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc 355																
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser 85																
gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa 403																
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu 100																
gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc 451																
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu 115																
ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca 499																
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala 130																
gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac 547																
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn 145																
ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc 595																
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr 165																
tcc gtc tac gac att qca aag ttg ctg cca cac tac gct ggc qga ctg 643																

Ser Val Tyr Asp Ile ^e Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu	
170	175 180
gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag	691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu	
185	190 195
gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc	739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile	
200	205 210
ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt	787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly	
215	220 225
ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag	835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln	
230	235 240 245
cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc	883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu	
250	255 260
gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca	931
Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala	
265	270 275
tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc	979
Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser	
280	285 290
atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag	1027
Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys	
295	300 305
aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc	1075
Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly	
310	315 320 325
cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc	1123
Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly	
330	335 340
atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc	1171
Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser	
345	350 355
gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg	1219
Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu	
360	365 370
aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc	1267
Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu	
375	380 385
gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag	1315
Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln	
390	395 400 405
taaatccgac acggcccttt gtt	1338

<210> 70
 <211> 405
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 70

```

Met Ala Val Lys Thr Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly
  1              5              10              15

Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp
      20              25              30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu
      35              40              45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
      50              55              60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val
      65              70              75              80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala
      85              90              95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
      100             105             110

Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr
      115             120             125

Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala
      130             135             140

Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
      145             150             155             160

His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His
      165             170             175

Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile
      180             185             190

Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys
      195             200             205

Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp
      210             215             220

Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln
      225             230             235             240

Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr
      245             250             255

Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val
      260             265             270

Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile
      275             280             285

```

Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400

Ala Ile Leu Ala Gln
 405

<210> 71

<211> 1398

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1375)

<223> RXA00235

<400> 71

cgaaacaaga ttcgtgcaac aattgggtgt agacgtgatt gaagacattt gatcacgtga 60

ataattctag ttagctccca agttggcata ggaggccaca gtg gct gaa atc atg 115
 Val Ala Glu Ile Met
 1 5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc 163
 His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
 10 15 20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt 211
 Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
 25 30 35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac 259
 Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
 40 45 50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac 307
 Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
 55 60 65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat 355
 Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70 75 80 85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac	403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
90 95 100	
aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt	451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
105 110 115	
gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc	499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
120 125 130	
ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc	547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile	
135 140 145	
acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg	595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met	
150 155 160 165	
atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc	643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly	
170 175 180	
gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	

aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc 1123
 Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
 330 335 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc 1171
 Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
 345 350 355

tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct 1219
 Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
 360 365 370

gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca 1267
 Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
 375 380 385

gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag 1315
 Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
 390 395 400 405

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca 1363
 Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
 410 415 420

cgc ttt cag ggc taaataaaaag cgcttttcga cgc 1398
 Arg Phe Gln Gly
 425

<210> 72

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
 1 5 10 15

Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
 20 25 30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
 35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
 50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
 65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
 85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
 100 105 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
 115 120 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
 130 135 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
 145 150 155 160
 Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
 165 170 175
 Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
 180 185 190
 Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
 195 200 205
 Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
 210 215 220
 Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
 225 230 235 240
 Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
 245 250 255
 Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
 260 265 270
 Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
 275 280 285
 Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
 290 295 300
 Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
 305 310 315 320
 Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
 325 330 335
 Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
 340 345 350
 Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
 355 360 365
 Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
 370 375 380
 Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
 385 390 395 400
 Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
 405 410 415
 Arg Ser Ala Phe Pro Arg Phe Gln Gly
 420 425

<210> 73

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA01093

<400> 73

```

cagaggcgta gaacattgtc tgttcacact ctgggtcgca agattcatcg agaattaatg 60

gtagtacctg tggcttgagg gggaaatgacg tactaggctt atg ggc gtg gat aga 115
                                         Met Gly Val Asp Arg
                                         1           5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
              10              15              20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
              25              30              35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
              40              45              50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac 307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
              55              60              65

ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc 355
Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
              70              75              80              85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
              90              95              100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac 451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
              105              110              115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc 499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
              120              125              130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag 547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
              135              140              145

ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat 595
Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
              150              155              160              165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc 643
Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
              170              175              180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc 691
Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
              185              190              195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt 739

```

Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met	Asp	Glu	Glu	Gly	Arg		
	200						205					210					
cgt	gtt	cct	gtg	atc	gcc	aag	ctg	gaa	aag	cca	gag	gct	gtc	acc	tcc	787	
Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	Glu	Ala	Val	Thr	Ser		
	215					220					225						
ctc	gag	cca	atc	gtg	ttg	gca	ttc	gac	gcc	gtc	atg	gtt	gct	cgt	ggc	835	
Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val	Met	Val	Ala	Arg	Gly		
230					235					240					245		
gac	ctc	ggc	gtt	gag	gtt	cct	ctg	gag	gag	gtt	cca	ctg	gtt	cag	aag	883	
Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val	Pro	Leu	Val	Gln	Lys		
			250						255					260			
cgc	gca	atc	cag	att	gcc	cgt	gag	aac	gca	aag	cca	gtt	atc	gtg	gca	931	
Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys	Pro	Val	Ile	Val	Ala		
		265						270					275				
acc	cag	atg	ctg	gat	tcc	atg	att	gag	aac	tcc	cgc	cca	acc	cgt	gcg	979	
Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser	Arg	Pro	Thr	Arg	Ala		
		280					285					290					
gaa	gct	tct	gac	gtg	gca	aac	gct	gtg	ctc	gat	ggc	gca	gat	gct	gtc	1027	
Glu	Ala	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp	Gly	Ala	Asp	Ala	Val		
	295					300					305						
atg	ctt	tct	ggc	gaa	act	tca	gtg	ggc	aaa	gat	ccg	cac	aac	gtt	gtg	1075	
Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	Pro	His	Asn	Val	Val		
310					315					320					325		
cgc	acc	atg	tct	cgc	att	gtt	cgc	ttc	gct	gaa	acc	gac	ggc	cgc	gtc	1123	
Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	Thr	Asp	Gly	Arg	Val		
				330					335					340			
cca	gac	ctg	acc	cac	atc	cct	cgc	act	aag	cgt	ggc	gtt	att	tcc	tac	1171	
Pro	Asp	Leu	Thr	His	Ile	Pro	Arg	Thr	Lys	Arg	Gly	Val	Ile	Ser	Tyr		
			345					350					355				
tct	gca	cgt	gat	atc	gcc	gag	cgc	ctc	aac	gct	cgt	gca	ttg	gtt	gcg	1219	
Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala	Arg	Ala	Leu	Val	Ala		
		360					365					370					
ttc	acc	acc	tct	ggc	gat	acc	gca	aag	cgt	gtg	gct	cgt	ctg	cac	agc	1267	
Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser		
		375				380					385						
cac	ctg	cca	ctg	ctc	gtg	ttc	act	cca	aac	gag	gca	gtt	cgc	tct	gag	1315	
His	Leu	Pro	Leu	Leu	Val	Phe	Thr	Pro	Asn	Glu	Ala	Val	Arg	Ser	Glu		
390					395					400					405		
ctg	gcg	ctg	acc	tgg	ggc	gca	acc	acc	ttc	ctg	tgt	cca	cct	gtc	agc	1363	
Leu	Ala	Leu	Thr	Trp	Gly	Ala	Thr	Thr	Phe	Leu	Cys	Pro	Pro	Val	Ser		
				410					415					420			
gat	acc	gat	gac	atg	atg	cgc	gaa	gtc	gac	cgt	gct	ctt	tta	gca	atg	1411	
Asp	Thr	Asp	Asp	Met	Met	Arg	Glu	Val	Asp	Arg	Ala	Leu	Leu	Ala	Met		
			425					430					435				
cct	gag	tac	aac	aag	ggc	gac	atg	atg	gtt	gtt	gtt	gca	ggc	tcc	cct	1459	
Pro	Glu	Tyr	Asn	Lys	Gly	Asp	Met	Met	Val	Val	Val	Ala	Gly	Ser	Pro		

440 445 450
 cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt 1507
 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
 455 460 465

 gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa 1554
 Asp Asp Thr Arg Ile Ala Lys Leu
 470 475

 <210> 74
 <211> 477
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 74
 Met Gly Val Asp Arg Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala
 1 5 10 15
 Val Ala Ser Ala Asp Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp
 20 25 30
 Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln
 35 40 45
 Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
 50 55 60
 Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65 70 75 80
 Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
 85 90 95
 Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
 100 105 110
 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
 115 120 125
 Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
 130 135 140
 Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
 145 150 155 160
 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
 165 170 175
 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
 180 185 190
 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
 195 200 205
 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
 210 215 220
 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
 225 230 235 240

Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
 245 250 255

Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
 260 265 270

Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
 275 280 285

Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
 290 295 300

Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
 305 310 315 320

Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
 325 330 335

Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
 340 345 350

Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
 355 360 365

Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
 370 375 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
 385 390 395 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
 405 410 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
 420 425 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
 435 440 445

Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His
 450 455 460

Val His Leu Leu Gly Asp Asp Thr Arg Ile Ala Lys Leu
 465 470 475

<210> 75

<211> 1980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1957)

<223> RXN02675

<400> 75

aagtgtttca ttggaacact tgcgctgcc aacttttgggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115

											Met	Asn	Glu	Phe	Asp	
											1					5
cag	gac	att	ctc	cag	gag	atc	aag	act	gaa	ctc	gac	gag	tta	att	cta	163
Gln	Asp	Ile	Leu	Gln	Glu	Ile	Lys	Thr	Glu	Leu	Asp	Glu	Leu	Ile	Leu	
				10					15					20		
gaa	ctt	gat	gag	gtg	aca	caa	act	cac	agc	gag	gcc	atc	ggg	cag	gtc	211
Glu	Leu	Asp	Glu	Val	Thr	Gln	Thr	His	Ser	Glu	Ala	Ile	Gly	Gln	Val	
			25					30					35			
tcc	cca	acc	cat	tac	gtt	ggt	gcc	cgc	aac	ctc	atg	cat	tac	gcg	cat	259
Ser	Pro	Thr	His	Tyr	Val	Gly	Ala	Arg	Asn	Leu	Met	His	Tyr	Ala	His	
		40					45					50				
ctt	cgc	acc	aaa	gac	ctc	cgt	ggc	ctg	cag	caa	cgc	ctc	tcc	tct	gtg	307
Leu	Arg	Thr	Lys	Asp	Leu	Arg	Gly	Leu	Gln	Gln	Arg	Leu	Ser	Ser	Val	
	55					60					65					
gga	gct	acc	cgc	ttg	act	acc	acc	gaa	cca	gca	gtg	cag	gcc	cgc	ctc	355
Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	Val	Gln	Ala	Arg	Leu	
	70				75			80							85	
aag	gcc	gcc	cgc	aat	gtt	atc	gga	gct	ttc	gca	ggt	gaa	ggc	cca	ctt	403
Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala	Gly	Glu	Gly	Pro	Leu	
				90				95						100		
tat	cca	ccc	tca	gat	gtc	gtc	gat	gcc	ttc	gaa	gat	gcc	gat	gag	att	451
Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile	
			105					110					115			
ctc	gac	gag	cac	gcc	gaa	att	ctc	ctt	ggc	gaa	ccc	cta	ccg	gat	act	499
Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu	Pro	Leu	Pro	Asp	Thr	
	120						125					130				
cca	tcc	tgc	atc	atg	gtc	acc	ctg	ccc	acc	gaa	gcc	gcc	acc	gac	att	547
Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile	
	135					140					145					
gaa	ctt	gtc	cgt	ggc	ttc	gcc	aaa	agc	ggc	atg	aat	cta	gct	cgc	atc	595
Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	Asn	Leu	Ala	Arg	Ile	
	150				155				160						165	
aac	tgt	gca	cac	gac	gat	gaa	acc	gtc	tgg	aag	cag	atg	atc	gac	aac	643
Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys	Gln	Met	Ile	Asp	Asn	
				170				175						180		
gtc	cac	acc	gtt	gca	gaa	gaa	gtt	ggc	cgg	gaa	atc	cgc	gtc	agc	atg	691
Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met	
			185					190					195			
gac	ctc	gcc	gga	cca	aaa	gta	cgc	acc	ggc	gaa	atc	gcc	cca	ggc	gca	739
Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala	
	200						205					210				
gaa	gta	ggt	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu	
	215					220					225					
acg	ccc	gca	aaa	ctg	tgg	atc	acc	gcc	cac	ggc	tcc	gaa	cca	gtc	cca	835
Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro	

230	235	240	245	
gcc ccc gaa agc ctg Ala Pro Glu Ser	ccc ggt cgc ccc gct ctg ccg att gaa gtc acc Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr			883
	250	255	260	
cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro		270	275	931
	265			
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp		285	290	979
	280			
ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly		300	305	1027
	295			
acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro		315	320	1075
	310		325	
gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu		330	335	1123
	330		340	
acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr		345	350	1171
	345		355	
cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val		360	365	1219
	360		370	
ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile		375	380	1267
	375		385	
gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val		390	395	1315
	390		400	405
acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile		410	415	1363
	410		420	
aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp		425	430	1411
	425		435	
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile		440	445	1459
	440		450	
tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu		455	460	1507
	455		465	
gcc gac atc gga gat cca gta gcc gtc gaa cgc ctt ggc ctc gtc ctt Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg Leu Gly Leu Val Leu		470	475	1555
	470		480	485

aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg 1603
 Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
 490 495 500

acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac 1651
 Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
 505 510 515

ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg 1699
 Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
 520 525 530

atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc 1747
 Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
 535 540 545

caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct cgc gca gaa 1795
 Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
 550 555 560 565

atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc atg ctg aac 1843
 Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
 570 575 580

aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
 Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
 585 590 595

cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
 Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
 600 605 610

gtg aag agc tgg gaa gag taactcacia aggcgattgg cgt 1980
 Val Lys Ser Trp Glu Glu
 615

<210> 76

<211> 619

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
 1 5 10 15

Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
 20 25 30

Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110
 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220
 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240
 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415

Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
 420 425 430

Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
 450 455 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
 465 470 475 480

Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
 485 490 495

Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
 500 505 510

Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
 515 520 525

Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
 530 535 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
 545 550 555 560

Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
 565 570 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
 580 585 590

Leu Thr Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg
 595 600 605

Leu Leu Leu Arg Lys Val Lys Ser Trp Glu Glu
 610 615

<210> 77

<211> 386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(363)

<223> FRXA02675

<400> 77

atc ctc atg acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc 48
 Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
 1 5 10 15

cgc gga gac ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc 96
 Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
 20 25 30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc 144
 Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile

35	40	45	
ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct			192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser			
50	55	60	
cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc			240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val			
65	70	75	80
atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc			288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr			
85	90	95	
gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg			336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu			
100	105	110	
ctg cgc aag gtg aag agc tgg gaa gag taactcacaa aggcgattgg			383
Leu Arg Lys Val Lys Ser Trp Glu Glu			
115	120		
cggt			386

<210> 78

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
1 5 10 15

Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
20 25 30

Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
35 40 45

Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
50 55 60

Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
65 70 75 80

Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
85 90 95

Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
100 105 110

Leu Arg Lys Val Lys Ser Trp Glu Glu
115 120

<210> 79

<211> 1522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1522)

<223> FRXA02695

<400> 79

```

aagtgtttca ttggaacact tgcgctgccca acttttttgggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115
                                         Met Asn Glu Phe Asp
                                         1           5

cag gac att ctc cag gag atc aag act gaa ctc gag gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
                10                15                20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
                25                30                35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
                40                45                50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
                55                60                65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
                70                75                80                85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
                90                95                100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
                105                110                115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
                120                125                130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
                135                140                145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
                150                155                160                165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
                170                175                180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
                185                190                195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca 739

```

Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala		
	200						205					210					
gaa	gta	ggg	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787	
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu		
	215					220					225						
acg	ccc	gca	aaa	ctg	tgg	atc	acc	gcc	cac	ggc	tcc	gaa	cca	gtc	cca	835	
Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro		
	230				235					240					245		
gcc	ccc	gaa	agc	ctg	ccc	ggg	cgc	ccc	gct	ctg	ccg	att	gaa	gtc	acc	883	
Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr		
				250				255						260			
cca	gaa	tgg	ttc	gac	aaa	cta	gaa	atc	ggc	agc	gtc	atc	aac	gtc	cca	931	
Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro		
			265					270					275				
gac	acc	cgc	gga	tcc	cgc	cga	gca	ttc	acc	gtg	acc	agg	gtt	ttt	gat	979	
Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp		
		280					285					290					
ggc	gcg	gtc	ctc	gcc	gaa	ggc	cca	caa	aaa	gcc	tac	atc	tcc	aac	ggc	1027	
Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly		
	295					300					305						
acc	ctc	ctg	gaa	cac	aac	tac	gac	cgc	tcc	cgg	gtc	tac	ggc	atc	ccc	1075	
Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro		
	310				315					320					325		
gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123	
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu		
				330					335					340			
acc	gac	gaa	gaa	ctc	acc	tac	gat	cca	tcc	ctc	gga	tcc	ggc	cgc	aca	1171	
Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr		
			345					350					355				
cca	cgc	atc	agc	tgc	acc	ctt	cca	caa	gca	gtc	gat	gca	att	aaa	gtc	1219	
Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val		
		360					365					370					
ggg	cac	cgc	gtg	ctt	ttc	gac	gac	gga	gcc	atc	gcc	gca	gtc	tgc	atc	1267	
Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile		
	375					380				385							
gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315	
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val		
	390				395					400				405			
acc	cac	gcc	cgc	cca	caa	ggc	gta	aac	ctg	gcc	gca	tac	aag	gga	atc	1363	
Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile		
				410				415						420			
aac	ctc	cca	gac	tcc	gaa	ctt	cca	ctc	cca	agc	ctc	act	gaa	gaa	gac	1411	
Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp		
			425					430					435				
ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459	
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile		

440 445 450
 tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc 1507
 Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
 455 460 465

 gcc gac atc gga gat 1522
 Ala Asp Ile Gly Asp
 470

 <210> 80
 <211> 474
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 80
 Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
 1 5 10 15
 Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
 20 25 30
 Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45
 Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60
 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80
 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95
 Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110
 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220
 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240

Ser	Glu	Pro	Val	Pro 245	Ala	Pro	Glu	Ser	Leu 250	Pro	Gly	Arg		Pro	Ala 255	Leu
Pro	Ile	Glu	Val 260	Thr	Pro	Glu	Trp	Phe 265	Asp	Lys	Leu	Glu		Ile 270	Gly	Ser
Val	Ile	Asn 275	Val	Pro	Asp	Thr	Arg 280	Gly	Ser	Arg	Arg	Ala 285		Phe	Thr	Val
Thr	Arg 290	Val	Phe	Asp	Gly	Ala 295	Val	Leu	Ala	Glu	Gly 300	Pro	Gln	Lys	Ala	
Tyr 305	Ile	Ser	Asn	Gly 310	Thr	Leu	Leu	Glu	His	Asn 315	Tyr	Asp	Arg	Ser	Arg 320	
Val	Tyr	Gly	Ile	Pro 325	Ala	Val	Val	Gln	Arg 330	Ile	Asn	Leu	Lys	Val 335	Gly	
Asp	Arg	Leu	Ile 340	Leu	Thr	Asp	Glu	Glu 345	Leu	Thr	Tyr	Asp	Pro 350	Ser	Leu	
Gly	Ser 355	Gly	Arg	Thr	Pro	Arg	Ile 360	Ser	Cys	Thr	Leu	Pro 365	Gln	Ala	Val	
Asp 370	Ala	Ile	Lys	Val	Gly	His 375	Arg	Val	Leu	Phe	Asp 380	Asp	Gly	Ala	Ile	
Ala 385	Ala	Val	Cys	Ile	Asp 390	Lys	Thr	Ser	Thr	Ala 395	Asp	Gly	His	Asn	Asp 400	
Val	Glu	Leu	Glu	Val 405	Thr	His	Ala	Arg	Pro 410	Gln	Gly	Val	Asn	Leu 415	Ala	
Ala	Tyr	Lys	Gly 420	Ile	Asn	Leu	Pro	Asp 425	Ser	Glu	Leu	Pro	Leu 430	Pro	Ser	
Leu	Thr 435	Glu	Glu	Asp	Leu	Gln	His 440	Leu	Arg	Phe	Val	Val 445	Lys	Tyr	Ala	
Asp 450	Ile	Ala	Ala	Ile	Ser	Phe 455	Ile	Arg	Asn	Val	Ala 460	Asp	Val	Glu	Tyr	
Leu 465	Leu	Gln	Ala	Leu	Ala 470	Asp	Ile	Gly	Asp							

```
<210> 81
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1999)  
<223> RXA00682
```

```
<400> 81
ataggcacct tcgatttcag ctcaatcacc gtcgcaatga ccggcacgaa gtaaaaccac 60
cgcatttttt cgtcqaaaaag catctaaaaag gaqtttgacc atg gct aat aaa tct 115
```

										Met	Ala	Asn	Lys	Ser		
										1				5		
ttc	ccc	aag	ccc	tcc	gat	ctt	cca	gtg	ccc	aag	ggc	gct	gaa	ggg	tgg	163
Phe	Pro	Lys	Pro	Ser	Asp	Leu	Pro	Val	Pro	Lys	Gly	Ala	Glu	Gly	Trp	
				10					15					20		
gaa	gat	ctg	tac	ccg	tac	tac	ctc	gtt	ttc	caa	gac	aag	ctc	atg	gat	211
Glu	Asp	Leu	Tyr	Pro	Tyr	Tyr	Leu	Val	Phe	Gln	Asp	Lys	Leu	Met	Asp	
				25					30					35		
caa	gag	aat	gag	aaa	ttc	tgg	ttc	tgc	gat	tca	cag	cac	tgg	cca	act	259
Gln	Glu	Asn	Glu	Lys	Phe	Trp	Phe	Cys	Asp	Ser	Gln	His	Trp	Pro	Thr	
				40					45					50		
gtg	ttc	aag	cct	ttt	gaa	act	atc	ggg	ggg	gaa	ttc	gct	gta	aag	tgc	307
Val	Phe	Lys	Pro	Phe	Glu	Thr	Ile	Gly	Gly	Glu	Phe	Ala	Val	Lys	Cys	
				55					60					65		
ctc	ggc	caa	tac	aac	gct	cgg	cat	ttg	atg	atc	ccg	aat	gcc	aat	ggc	355
Leu	Gly	Gln	Tyr	Asn	Ala	Arg	His	Leu	Met	Ile	Pro	Asn	Ala	Asn	Gly	
				70					75					80		
atc	gag	ttc	cgc	gtg	cat	ctg	gga	tac	ctc	tat	atg	tcc	cct	att	cca	403
Ile	Glu	Phe	Arg	Val	His	Leu	Gly	Tyr	Leu	Tyr	Met	Ser	Pro	Ile	Pro	
				90					95					100		
gtg	cct	gaa	gat	cag	att	gcg	gaa	cgc	gtc	ccc	atg	ttc	cag	gaa	cgc	451
Val	Pro	Glu	Asp	Gln	Ile	Ala	Glu	Arg	Val	Pro	Met	Phe	Gln	Glu	Arg	
				105					110					115		
atc	acg	cac	tac	ttc	caa	aac	tgg	gag	cca	atg	ctg	gca	aat	tgg	aag	499
Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met	Leu	Ala	Asn	Trp	Lys	
				120					125					130		
gag	cga	gta	tta	gga	acc	atc	aat	gag	ctg	gaa	tct	cta	gaa	ttc	aag	547
Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu	Ser	Leu	Glu	Phe	Lys	
				135					140					145		
cca	ctg	cct	gac	tac	gtg	cct	atc	gat	gat	att	gtc	tcc	gga	aaa	gcc	595
Pro	Leu	Pro	Asp	Tyr	Val	Pro	Ile	Asp	Asp	Ile	Val	Ser	Gly	Lys	Ala	
				150					155					160		
aaa	gac	ggc	acc	gaa	gta	ctc	atg	gaa	aac	ttc	gat	cgg	ctc	att	cag	643
Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe	Asp	Arg	Leu	Ile	Gln	
				170					175					180		
ctc	gcc	tac	caa	aac	tgg	caa	tac	cac	ttt	gag	ttc	ctc	aac	ttg	ggg	691
Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu	Phe	Leu	Asn	Leu	Gly	
				185					190					195		
tac	atc	gct	tac	cta	gat	ttc	ttc	aat	ttc	tgc	aag	gaa	gtc	ttc	cca	739
Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys	Lys	Glu	Val	Phe	Pro	
				200					205					210		
gat	atc	cct	gat	caa	tca	att	tcg	atg	atg	gtt	cag	ggc	gtg	gat	atg	787
Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val	Gln	Gly	Val	Asp	Met	
				215					220					225		
gag	ctg	ttc	cgc	ccc	gat	gat	gaa	cta	aag	att	ctg	gca	cag	cta	gcg	835
Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile	Leu	Ala	Gln	Leu	Ala	

230	235	240	245	
gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa	883			
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln				
250 255 260				
gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata	931			
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile				
265 270 275				
gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt	979			
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly				
280 285 290				
aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt	1027			
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu				
295 300 305				
cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa	1075			
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln				
310 315 320 325				
acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg	1123			
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val				
330 335 340				
gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt	1171			
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe				
345 350 355				
gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac	1219			
Asp Ala Lys Cys Gly Leu Ala Thr Ala Tyr Pro Tyr Val Glu Asn				
360 365 370				
cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa	1267			
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys				
375 380 385				
gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac	1315			
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn				
390 395 400 405				
gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc	1363			
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu				
410 415 420				
ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att	1411			
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile				
425 430 435				
ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc	1459			
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val				
440 445 450				
acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca	1507			
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro				
455 460 465				
gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc	1555			
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr				
470 475 480 485				

gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga 1603
 Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
 490 495 500

acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct 1651
 Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
 505 510 515

cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa 1699
 Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
 520 525 530

atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc 1747
 Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
 535 540 545

aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct 1795
 Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
 550 555 560 565

gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc 1843
 Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
 570 575 580

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga 1891
 Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
 585 590 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
 600 605 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg 1987
 Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
 615 620 625

gat aca cat gcc tagtccacgc actgtttctta tca 2022
 Asp Thr His Ala
 630

<210> 82

<211> 633

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ala Asn Lys Ser Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys
 1 5 10 15

Gly Ala Glu Gly Trp Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln
 20 25 30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
 35 40 45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
 50 55 60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile

65					70						75				80
Pro	Asn	Ala	Asn	Gly	Ile	Glu	Phe	Arg	Val	His	Leu	Gly	Tyr	Leu	Tyr
				85					90					95	
Met	Ser	Pro	Ile	Pro	Val	Pro	Glu	Asp	Gln	Ile	Ala	Glu	Arg	Val	Pro
			100					105					110		
Met	Phe	Gln	Glu	Arg	Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met
		115					120					125			
Leu	Ala	Asn	Trp	Lys	Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu
	130					135					140				
Ser	Leu	Glu	Phe	Lys	Pro	Leu	Pro	Asp	Tyr	Val	Pro	Ile	Asp	Asp	Ile
145					150					155					160
Val	Ser	Gly	Lys	Ala	Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe
				165					170					175	
Asp	Arg	Leu	Ile	Gln	Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu
			180					185					190		
Phe	Leu	Asn	Leu	Gly	Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys
		195					200					205			
Lys	Glu	Val	Phe	Pro	Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val
	210					215					220				
Gln	Gly	Val	Asp	Met	Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile
225					230					235					240
Leu	Ala	Gln	Leu	Ala	Val	Asp	Leu	Gly	Leu	Gln	Thr	His	Phe	Ala	Asn
				245					250					255	
Pro	Asp	Asp	Pro	Gln	Ala	Thr	Leu	Ala	Ala	Ile	Ala	Lys	Ala	Glu	Gly
			260					265					270		
Gly	Ala	Thr	Trp	Ile	Ala	Arg	Trp	Glu	Glu	Ala	Gln	Asp	Pro	Trp	Phe
		275					280					285			
Asn	Phe	Thr	Val	Gly	Asn	Gly	Phe	Tyr	Gly	His	Asp	Lys	Tyr	Trp	Ile
	290					295					300				
Glu	His	Leu	Glu	Leu	Pro	Leu	Gly	Tyr	Ile	Ala	Asp	Tyr	Ile	Arg	Arg
305					310					315					320
Leu	Asp	Glu	Gly	Gln	Thr	Ile	Ser	Arg	Pro	Lys	Asp	Glu	Leu	Ile	Ala
				325					330					335	
Glu	Lys	Glu	Arg	Val	Val	Glu	Glu	Tyr	Arg	Asp	Leu	Leu	Asp	Gly	Glu
			340					345					350		
Gln	Leu	Ala	Gln	Phe	Asp	Ala	Lys	Cys	Gly	Leu	Ala	Ala	Thr	Ala	Tyr
		355					360					365			
Pro	Tyr	Val	Glu	Asn	His	Asn	Phe	Tyr	Ile	Glu	His	Trp	Thr	Met	Ser
	370					375					380				
Val	Phe	Trp	Arg	Lys	Val	Arg	Glu	Leu	Ser	Arg	Thr	Leu	Gln	Gly	Tyr
385					390					395					400

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
 405 410 415
 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
 420 425 430
 Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
 435 440 445
 Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
 450 455 460
 Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
 465 470 475 480
 Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
 485 490 495
 Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
 500 505 510
 Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
 515 520 525
 Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
 530 535 540
 Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
 545 550 555 560
 Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
 565 570 575
 Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
 580 585 590
 Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
 595 600 605
 Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
 610 615 620
 Ala Ala His Gly Val Asp Thr His Ala
 625 630

<210> 83

<211> 1215

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1192)

<223> RXA00683

<400> 83

ggacaaagct atcgggttcc gggagaacct ctccttcogc gtcccccactt ctgttcccgt 60

gacttggaac gcttaacgct ttattaaata aggagacacc atg acc aac agt ttg 115

											Met 1	Thr	Asn	Ser	Leu 5	
aac Asn	atc Ile	ccg Pro	ttt Phe	gtc Val 10	cag Gln	cgc Arg	ttc Phe	gat Asp	gaa Glu 15	ggc Gly	ctg Leu	gat Asp	cct Pro	gtt Val 20	cta Leu	163
gaa Glu	gta Val	ctc Leu	ggg Gly 25	ggc Gly	aag Lys	ggc Gly	gct Ala	tca Ser 30	cta Leu	gtc Val	acc Thr	atg Met	aca Thr 35	gat Asp	gct Ala	211
gga Gly	atg Met	ccc Pro 40	gtt Val	cca Pro	cct Pro	gga Gly	ttt Phe 45	gtg Val	gtc Val	act Thr	act Thr	gcc Ala 50	agc Ser	ttt Phe	gat Asp	259
gaa Glu	ttc Phe 55	atc Ile	cgt Arg	gaa Glu	gca Ala	ggg Gly 60	gtt Val	gct Ala	gaa Glu	cac His	atc Ile 65	gat Asp	aaa Lys	ttc Phe	cta Leu	307
aac Asn 70	gat Asp	ctc Leu	gat Asp	gca Ala	gaa Glu 75	gat Asp	gtt Val	aag Lys	gaa Glu	gtg Val 80	gat Asp	cga Arg	gtt Val	tct Ser	gcg Ala 85	355
atc Ile	atc Ile	cgc Arg	gat Asp	gag Glu 90	ctg Leu	tgc Cys	agt Ser	ctt Leu	gac Asp 95	gtt Val	cca Pro	gag Glu	aat Asn	gct Ala 100	cgt Arg	403
ttc Phe	gca Ala	gtg Val	cac His 105	cag Gln	gct Ala	tat Tyr	cgc Arg	gat Asp 110	ctc Leu	atg Met	gaa Glu	cga Arg	tgc Cys 115	ggg Gly	ggc Gly	451
gac Asp	gtc Val	ccg Pro 120	gtt Val	gct Ala	gtc Val	cgg Arg	tca Ser 125	tcg Ser	gcc Ala	act Thr	gcc Ala	gaa Glu 130	gat Asp	ctg Leu	ccc Pro	499
gat Asp	gct Ala	tcc Ser	ttc Phe	gca Ala	ggg Gly	caa Gln 140	cag Gln	gac Asp	acc Thr	tat Tyr	ctg Leu 145	tgg Trp	caa Gln	gtc Val	ggg Gly	547
ttg Leu 150	agc Ser	gct Ala	gtc Val	act Thr	gaa Glu 155	cac His	atc Ile	cgt Arg	aaa Lys	tgc Cys 160	tgg Trp	gct Ala	tcg Ser	ctg Leu	ttc Phe 165	595
act Thr	tcc Ser	cgt Arg	gcc Ala	att Ile 170	atc Ile	tac Tyr	cgt Arg	ctg Leu	aaa Lys 175	aac Asn	aac Asn	atc Ile	ccc Pro	aat Asn 180	gag Glu	643
ggc Gly	ctc Leu	tcc Ser	atg Met 185	gcg Ala	gta Val	gtt Val	gtt Val	caa Gln 190	aaa Lys	atg Met	gtc Val	aac Asn	tct Ser	cgt Arg	gtc Val	691
gca Ala	ggc Gly	gtg Val 200	gca Ala	atc Ile	act Thr	atg Met	aat Asn 205	cct Pro	tcc Ser	aac Asn	ggc Gly	gac Asp 210	cgc Arg	tcg Ser	aag Lys	739
atc Ile	acc Thr 215	atc Ile	gat Asp	tcc Ser	tca Ser	tgg Trp 220	ggg Gly	gtt Val	ggg Gly	gaa Glu	atg Met 225	gtg Val	gtc Val	tca Ser	ggg Gly	787
gaa Glu	gtg Val	aca Thr	cca Pro	gac Asp	aat Asn	atc Ile	ttg Leu	ctg Leu	gac Asp	aag Lys	atc Ile	acg Thr	ctg Leu	cag Gln	gtt Val	835

230	235	240	245	
gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc	883			
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala				
250 255 260				
acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac	931			
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn				
265 270 275				
cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct	979			
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala				
280 285 290				
aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg	1027			
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala				
295 300 305				
ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc	1075			
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser				
310 315 320 325				
cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act	1123			
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr				
330 335 340				
ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc	1171			
Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr				
345 350 355				
gtc gca atg acc ggc acg aag taaaaccacc gcacatcttttc gtc	1215			
Val Ala Met Thr Gly Thr Lys				
360				

<210> 84

<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Thr Asn Ser Leu Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly	
1 5 10 15	
Leu Asp Pro Val Leu Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val	
20 25 30	
Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr	
35 40 45	
Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His	
50 55 60	
Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val	
65 70 75 80	
Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val	
85 90 95	
Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met	
100 105 110	

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
 115 120 125
 Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
 130 135 140
 Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
 145 150 155 160
 Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
 165 170 175
 Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
 180 185 190
 Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
 195 200 205
 Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
 210 215 220
 Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
 225 230 235 240
 Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
 245 250 255
 Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
 260 265 270
 Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
 275 280 285
 Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
 290 295 300
 Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
 305 310 315 320
 Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
 325 330 335
 Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp
 340 345 350
 Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
 355 360

<210> 85

<211> 1860

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1837)

<223> RXN00635

<400> 85

```

ctggcaggcg ggcgaagcgt ggcaacaact ggaatttaag agcacaattg aagtcgcacc 60

aagttaggca acacaatagc cataacgttg aggagttcag atg gca cac agc tac 115
                                         Met Ala His Ser Tyr
                                         1 5

gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att 163
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
                        10 15 20

tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc 211
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
                        25 30 35

caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg 259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
                        40 45 50

ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt 307
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
                        55 60 65

gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat 355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
                        70 75 80 85

gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att 403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
                        90 95 100

ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag 451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
                        105 110 115

att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt 499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
                        120 125 130

gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg 547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
                        135 140 145

ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa 595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
                        150 155 160 165

gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act 643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
                        170 175 180

cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg 691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
                        185 190 195

att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag 739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
                        200 205 210

aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg 787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
                        215 220 225

```


atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg	835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro	
230 235 240 245	
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat	883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	
250 255 260	
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct	931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	
265 270 275	
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac	979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	
280 285 290	
ggg gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt	1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	
295 300 305	
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa	1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	
310 315 320 325	
aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag	1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys	
330 335 340	
ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg	1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
345 350 355	
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat	1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp	
360 365 370	
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat	1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
375 380 385	
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca	1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser	
390 395 400 405	
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg	1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
410 415 420	
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt	1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly	
425 430 435	
ggg ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa	1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln	
440 445 450	
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg	1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val	
455 460 465	

```

aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat 1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
470 475 480 485

gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg 1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser
490 495 500

gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca 1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
505 510 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat 1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
520 525 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc 1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
535 540 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg 1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550 555 560 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca 1837
Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
570 575

tgatgattga tacacctgct gtt 1860

```

<210> 86

<211> 579

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

```

Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
 1 5 10 15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
20 25 30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

```

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
 145 150 155 160
 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
 165 170 175
 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
 180 185 190
 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
 195 200 205
 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
 210 215 220
 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
 225 230 235 240
 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
 245 250 255
 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
 260 265 270
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 275 280 285
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 290 295 300
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 305 310 315 320
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 325 330 335
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 340 345 350
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 355 360 365
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 370 375 380
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 385 390 395 400
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 405 410 415
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 420 425 430
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 435 440 445
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser

450	455	460
Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu		
465	470	475 480
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala		
	485	490 495
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu		
	500	505 510
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile		
	515	520 525
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu		
	530	535 540
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly		
	545	550 555 560
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile		
	565	570 575
Pro Thr Pro		

<210> 87
 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(552)
 <223> FRXA02807

<400> 87
 aaagcgtggc aacaactgga atttaagagc acaattgaag tcgcaccaag ttaggcaaca 60
 caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta 114
 Met Ala His Ser Tyr Ala Glu Gln Leu
 1 5
 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10 15 20 25
 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 210
 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 30 35 40
 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 45 50 55
 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 60 65 70
 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 354

Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg
 75 80 85
 aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag 402
 Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
 90 95 100 105
 att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag 450
 Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
 110 115 120
 gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa 498
 Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
 125 130 135
 cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg 546
 Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
 140 145 150
 tcg gtg 552
 Ser Val
 155

<210> 88

<211> 155

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 88

Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
 1 5 10 15
 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30
 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45
 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 50 55 60
 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65 70 75 80
 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 85 90 95
 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 100 105 110
 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
 115 120 125
 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
 145 150 155

<210> 89
 <211> 944
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(921)
 <223> FRXA00635

<400> 89
 ggt acg gat ttc cct tat tct gat ttc ctt cct aaa gac aac gtt gcc 48
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 1 5 10 15
 cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 20 25 30
 tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 35 40 45
 cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 50 55 60
 gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac 240
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65 70 75 80
 gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg 288
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 85 90 95
 aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg 336
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 100 105 110
 tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc 384
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 115 120 125
 gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct 432
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg 480
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc 528
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt 576
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa 624
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu

195	200	205	
ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct			672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
210	215	220	
gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag			720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
225	230	235	240
cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc			768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
245	250	255	
gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa			816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
260	265	270	
cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga			864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
275	280	285	
gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att			912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
290	295	300	
cct act cca tgatgattga tacacctgct gtt			944
Pro Thr Pro			
305			

<210> 90

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala			
1	5	10	15
Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys			
20	25	30	
Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro			
35	40	45	
His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys			
50	55	60	
Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn			
65	70	75	80
Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu			
85	90	95	
Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met			
100	105	110	
Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg			
115	120	125	

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
 275 280 285
 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
 290 295 300
 Pro Thr Pro
 305

<210> 91
 <211> 954
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXN03044

<400> 91
 tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60
 ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc 115
 Met Ala Arg Gly Phe
 1 5
 ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
 10 15 20
 cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt	259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
40 45 50	
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt	307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
55 60 65	
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag	355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
70 75 80 85	
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac	403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	
90 95 100	
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt	451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	
105 110 115	
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac	499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	
120 125 130	
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg	547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
135 140 145	
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt	595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	
150 155 160 165	
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc	643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser	
170 175 180	
ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag	691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln	
185 190 195	
atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc	739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
200 205 210	
ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc	787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile	
215 220 225	
gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa	835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu	
230 235 240 245	
ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag	883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys	
250 255 260	
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa	931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu	
265 270 275	

taaatacacct caaggacag ata

954

<210> 92

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
 1 5 10 15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
 20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
 245 250 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
 260 265 270

Asn Ala Pro Glu Glu

275

<210> 93
 <211> 302
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(279)
 <223> FRXA02852

<400> 93
 gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15
 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90
 caaggacag ata 302

<210> 94
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 94
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
85 90

<210> 95
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> FRXA00268

<400> 95
tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60
ccagcgcacc ggtgactcca tttgggcagc agccgatcag atg gca cgt ggc ttc 115
Met Ala Arg Gly Phe
1 5
ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc 163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Leu Thr Gly Glu Gly Leu
10 15 20
cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt 211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
25 30 35
gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt 259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
40 45 50
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt 307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
55 60 65
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag 355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
70 75 80 85
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac 403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
90 95 100
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt 451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
105 110 115
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac 499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
120 125 130
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg 547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
135 140 145
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt 595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150 155 160 165

gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc 643
 Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
 170 175 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
 185 190 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc 739
 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
 200 205 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc 787
 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
 215 220 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
 230 235 240 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
 250 255 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
 Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 265 270 275

taaatcacct caaggacag ata 954

<210> 96

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

Met Ala Arg Gly Phe Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
 1 5 10 15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
 20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140
 Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160
 Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175
 Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190
 Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205
 Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220
 Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240
 Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
 245 250 255
 Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
 260 265 270
 Asn Ala Pro Glu Glu
 275

<210> 97
 <211> 508
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(508)
 <223> RXN03086

<400> 97
 ttcggtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60
 cgtataaacg aaataaaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

```

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
    55                60                65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
    70                75                80                85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
                90                95                100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
        105                110                115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
        120                125                130

ggc gca gcc
Gly Ala Ala
    135

```

<210> 98
 <211> 136
 <212> PRT
 <213> *Corynebacterium glutamicum*

```

<400> 98
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
  1          5          10          15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
        20                25                30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
        35                40                45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
        50                55                60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
        65                70                75                80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
        85                90                95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
        100                105                110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
        115                120                125

Ile Ser Thr Tyr Ala Gly Ala Ala
        130                135

```

<210> 99
 <211> 508

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> FRXA02887

<400> 99

ttcgtgcact tcggcgtgcc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg	aaataaaaaca	ttccaacagg	aggtgtggaa	atg gcc gat caa gca	115
				Met Ala Asp Gln Ala	
				1 5	

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc	163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg	
10 15 20	

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac	211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn	
25 30 35	

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa	259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu	
40 45 50	

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag	307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys	
55 60 65	

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att	355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile	
70 75 80 85	

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag	403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys	
90 95 100	

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc	451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg	
105 110 115	

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca	499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala	
120 125 130	

ggc gca gcc	508
Gly Ala Ala	
135	

<210> 100

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
1 5 10 15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30
 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110
 Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
 115 120 125
 Ile Ser Thr Tyr Ala Gly Ala Ala
 130 135

<210> 101
 <211> 1385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1362)
 <223> RXN03043

<400> 101
 gat ctc gat ggc ttc cgt cag gaa gtt tcc cgt gag cag ggt ggc att 48
 Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
 1 5 10 15
 ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336

Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly		
			100					105					110				
aac	acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggc	gca	ggc	384	
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly		
		115					120					125					
tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggg	cgc	gag	tgg	gat	gaa	ctt	ctg	432	
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu		
		130					135					140					
gag	aag	gac	cag	gat	ggg	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480	
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser		
145					150				155						160		
gat	ggg	gac	tac	cag	acc	ttc	aag	gct	aac	gac	ggc	gca	tat	gtt	cgt	528	
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg		
				165				170						175			
gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576	
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn		
			180					185					190				
atg	acc	gac	gaa	gaa	atc	tgg	aag	ctt	cca	cgt	ggc	ggc	cac	gat	tac	624	
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr		
		195					200					205					
cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672	
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg		
		210				215					220						
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720	
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His		
225					230					235					240		
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768	
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu		
				245				250						255			
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816	
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp		
			260					265					270				
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggg	864	
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly		
		275					280					285					
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912	
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu		
		290				295					300						
ggg	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960	
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val		
305					310					315					320		
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008	
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln		
				325					330					335			
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056	
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met		

340	345	350	
cgc gat aag ggc ttg gct gat	cgc ctt gtc cca atc att cct gat gag	1104	
Arg Asp Lys Gly Leu Ala Asp	Arg Leu Val Pro Ile Ile Pro Asp Glu		
355	360	365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152		
Ala Arg Thr Phe Gly Leu Asp	Ser Trp Phe Pro Thr Leu Lys Ile Tyr		
370	375	380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200		
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu			
385	390	395	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248		
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn			
405	410	415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc tcc tac gcc	1296		
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala			
420	425	430	
acc cac ggc aag gcc atg att ccg ctg tac atc ttc tac tcg atg ttc	1344		
Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe			
435	440	445	
ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg	1385		
Gly Ile Pro Ala His Arg			
450			

<210> 102

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
1 5 10 15

Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
20 25 30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
35 40 45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
65 70 75 80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
85 90 95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
100 105 110

Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
115 120 125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
 420 425 430
 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
 435 440 445
 Gly Ile Pro Ala His Arg

450

<210> 103

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1287)

<223> FRXA02897

<400> 103

gat	ctc	gat	ggc	ttc	cgt	cag	gaa	gtt	tcc	cgt	gag	cag	ggt	ggc	att	48
Asp	Leu	Asp	Gly	Phe	Arg	Gln	Glu	Val	Ser	Arg	Glu	Gln	Gly	Gly	Ile	
1				5					10					15		

cgc	tcc	tac	cct	cac	cca	cac	ggt	atg	aag	gac	ttc	tgg	gag	ttc	cca	96
Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Lys	Asp	Phe	Trp	Glu	Phe	Pro	
			20					25					30			

act	gtg	tcc	atg	ggt	ctt	ggc	cca	atg	gat	gcc	att	tac	cag	gca	cgt	144
Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	Ala	Ile	Tyr	Gln	Ala	Arg	
			35				40					45				

ttc	aac	cgc	tac	ctc	gaa	aac	cgt	ggc	atc	aag	gac	acc	tct	gac	cag	192
Phe	Asn	Arg	Tyr	Leu	Glu	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Asp	Gln	
	50					55					60					

cac	gtc	tgg	gcc	ttc	ctt	ggc	gac	ggc	gaa	atg	gac	gag	cca	gaa	tca	240
His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser	
65					70				75						80	

cgt	ggt	ctc	atc	cag	cag	gct	gca	ctg	aac	aac	ctg	gac	aac	ctg	acc	288
Arg	Gly	Leu	Ile	Gln	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr	
				85					90					95		

ttc	gtg	gtt	aac	tgc	aac	ctg	cag	cgt	ctc	gac	gga	cct	gtc	cgc	ggt	336
Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	
			100					105					110			

aac	acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggc	gca	ggc	384
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	
		115					120					125				

tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggt	cgc	gag	tgg	gat	gaa	ctt	ctg	432
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	
		130				135						140				

gag	aag	gac	cag	gat	ggt	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser	
145					150					155					160	

gat	ggt	gac	tac	cag	acc	ttc	aag	gct	aac	gac	ggc	gca	tat	gtt	cgt	528
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	
				165					170					175		

gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn	
			180					185						190		

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
195 200 205	
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
210 215 220	
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
225 230 235 240	
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
275 280 285	
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
290 295 300	
ggg ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
340 345 350	
cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
355 360 365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
370 375 380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
385 390 395 400	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
405 410 415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc	1287
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr	
420 425	

<210> 104
 <211> 429
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 104
 Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
 1 5 10 15
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285

Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
 420 425

<210> 105
 <211> 1133
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (88)..(1110)
 <223> RXN03083

<400> 105
 attcagcagt aatcatttag acttggaacc gcttaccagt gggttcaaca atgcattcac 60
 ccagctcaca cgtgtggagg tgccttaatg gca aag agg atc gta att atc ggc 114
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac	354
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp	
75 80 85	
ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca	402
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser	
90 95 100 105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc	450
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr	
110 115 120	
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	498
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu	
125 130 135	
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	546
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro	
140 145 150	
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	594
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp	
155 160 165	
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val	
170 175 180 185	
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu	
190 195 200	
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His	
205 210 215	
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	786
Asp Asp Ala Asp Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg	
220 225 230	
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr	
235 240 245	
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr	
250 255 260 265	
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp	
270 275 280	
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc	978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile	
285 290 295	
aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag	1026
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln	
300 305 310	
gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg	1074

Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325

gcc gta tcg cca tgt atc acg cac tcg gtg aag gcg tgagcccat 1120

Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
 330 335 340

ccgtttgaag act 1133

<210> 106

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
 1 5 10 15

Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
 20 25 30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240

Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
 275 280 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
 290 295 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
 305 310 315 320

His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
 325 330 335

His Ser Val Lys Ala
 340

<210> 107
 <211> 1518
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (89)..(1495)
 <223> FRXA02853

<400> 107
 aattcagcag taatcattta gacttggaac cgcttaccag tggtttcaac aatgcattca 60
 cccagctcac acgtgtggag gtgccttaatg gca aag agg atc gta att atc ggc 115
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25

gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
 75 80 85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser

90	95	100	105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr	110	115	120	451
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu	125	130	135	499
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro	140	145	150	547
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp	155	160	165	595
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val	170	175	180	643
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu	190	195	200	691
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His	205	210	215	739
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg	220	225	230	787
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr	235	240	245	835
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr	250	255	260	883
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp	270	275	280	931
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile	285	290	295	979
aag gtt gac cgn gtc tcc cgc acc aac atc ccc ggt gtg tac gca gca Lys Val Asp Arg Val Ser Arg Thr Asn Ile Pro Gly Val Tyr Ala Ala	300	305	310	1027
ggt gac tgt act gac cta ttc cca ctg gcg tcc gtt gca gcg atg cag Gly Asp Cys Thr Asp Leu Phe Pro Leu Ala Ser Val Ala Ala Met Gln	315	320	325	1075
ggc cgt atc gcc atg tat cac gca ctc ggt gaa ggc gtg agc ccc atc Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile	330	335	340	1123

cgt ttg aag act gtt gcc acc gca gtg ttt acc cgc cca gag atc gca 1171
 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala 360
 350 355

gca gta ggt atc acc cat gca caa gtt gat tcc ggc gaa gtg tct gct 1219
 Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala 375
 365 370

cgc gtg att gtg ctt cct ttg gct act aac cca cgc gcc aag atg cgt 1267
 Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg 390
 380 385

tcc ctg cgc cac ggt ttt gtg aag ctg ttc tgc cgc cgt aac tct ggc 1315
 Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly 405
 395 400

ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc 1363
 Leu Ile Ile Gly Gly Val Val Val Ala Pro Thr Ala Ser Glu Leu Ile 425
 410 415 420

cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg 1411
 Leu Pro Ile Ala Val Ala Val Thr Asn Arg Leu Thr Val Ala Asp Leu 440
 430 435

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu 455
 445 450

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505
 Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly 465
 460

gagtcttaga ttt 1518

<210> 108

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
1 5 10 15

Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
20 25 30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly

100					105					110					
Val	Gly	Arg	Phe	Asp	Asp	Tyr	Asn	Thr	Lys	Gln	Thr	Thr	His	Tyr	Ile
		115					120					125			
Lys	Val	Thr	His	Ser	Asp	Gly	Ser	Glu	Glu	Thr	Val	Glu	Cys	Asp	Leu
	130					135					140				
Val	Leu	Val	Ala	Thr	Gly	Ala	Thr	Pro	Arg	Ile	Leu	Lys	Gly	Ala	Glu
145					150					155					160
Pro	Asp	Gly	Glu	Arg	Ile	Leu	Thr	Trp	Arg	Gln	Val	Tyr	Asp	Ile	Glu
				165					170					175	
Glu	Leu	Pro	Thr	His	Leu	Ile	Val	Val	Gly	Ser	Gly	Val	Thr	Gly	Ala
			180					185					190		
Glu	Phe	Val	Ser	Ala	Phe	Ala	Glu	Leu	Gly	Val	Lys	Val	Thr	Met	Val
		195					200					205			
Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His	Asp	Asp	Ala	Asp	Ala	Ala	Asp
	210					215					220				
Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg	Gly	Val	Ser	Leu	Glu	Lys	His
225					230					235					240
Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr	Glu	Asp	Gly	Gly	Val	Cys	Val
				245					250					255	
Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr	Gly	Ser	His	Ala	Leu	Met	Thr
			260					265					270		
Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp	Leu	Gly	Leu	Glu	Asn	Ile	Gly
		275					280					285			
Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile	Lys	Val	Asp	Arg	Val	Ser	Arg
	290					295					300				
Thr	Asn	Ile	Pro	Gly	Val	Tyr	Ala	Ala	Gly	Asp	Cys	Thr	Asp	Leu	Phe
305					310					315					320
Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln	Gly	Arg	Ile	Ala	Met	Tyr	His
				325					330					335	
Ala	Leu	Gly	Glu	Gly	Val	Ser	Pro	Ile	Arg	Leu	Lys	Thr	Val	Ala	Thr
			340					345					350		
Ala	Val	Phe	Thr	Arg	Pro	Glu	Ile	Ala	Ala	Val	Gly	Ile	Thr	His	Ala
		355					360					365			
Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala	Arg	Val	Ile	Val	Leu	Pro	Leu
	370					375					380				
Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg	Ser	Leu	Arg	His	Gly	Phe	Val
385					390					395					400
Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly	Leu	Ile	Ile	Gly	Gly	Val	Val
				405					410					415	
Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile	Leu	Pro	Ile	Ala	Val	Ala	Val
			420					425					430		

Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
 435 440 445

Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln
 450 455 460

His Asp Asp Leu Gly
 465

<210> 109

<211> 2895

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2872)

<223> RXA02259

<400> 109

atgagcccat gaaagccatc gaaatcaatc gccagctaa acacctgttt tgctgggtga 60

ttttttatct catgcacgcc aacaccctca atgtgaaaga gtg ttt aaa gta gtt 115
 Val Phe Lys Val Val
 1 5

atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc 163
 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
 10 15 20

ggg gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211
 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
 25 30 35

gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa 259
 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
 40 45 50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307
 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
 55 60 65

aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355
 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
 70 75 80 85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403
 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
 90 95 100

ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451
 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
 105 110 115

aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat 499
 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
 120 125 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc 547

Ala	Glu	Val	Ala	Pro	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Thr	Arg	Arg		
135						140					145						
cgc	act	gtt	ttt	gat	gcg	caa	aag	tgg	atc	acc	acc	cac	atg	cgt	gaa	595	
Arg	Thr	Val	Phe	Asp	Ala	Gln	Lys	Trp	Ile	Thr	Thr	His	Met	Arg	Glu		
150					155					160					165		
cgc	cac	gct	ttg	cag	tct	gcg	gag	cct	acc	gct	cgt	acg	caa	agc	aag	643	
Arg	His	Ala	Leu	Gln	Ser	Ala	Glu	Pro	Thr	Ala	Arg	Thr	Gln	Ser	Lys		
				170					175					180			
ttg	gat	gag	atc	gag	aag	aac	atc	cgc	cgt	cgc	atc	acc	att	ttg	tgg	691	
Leu	Asp	Glu	Ile	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Ile	Thr	Ile	Leu	Trp		
			185					190					195				
cag	acc	gcg	ttg	att	cgt	gtg	gcc	cgc	cca	cgt	atc	gag	gac	gag	atc	739	
Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
		200					205					210					
gaa	gta	ggg	ctg	cgc	tac	tac	aag	ctg	agc	ctt	ttg	gaa	gag	att	cca	787	
Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Ile	Pro		
		215				220					225						
cgt	atc	aac	cgt	gat	gtg	gct	gtt	gag	ctt	cgt	gag	cgt	ttc	ggc	gag	835	
Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	Arg	Glu	Arg	Phe	Gly	Glu		
230					235					240					245		
ggg	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggg	tcc	tgg	att	ggg	gga	883	
Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly	Ser	Trp	Ile	Gly	Gly		
				250					255					260			
gac	cac	gac	ggg	aac	cct	tat	gtc	acc	gcg	gaa	aca	gtt	gag	tat	tcc	931	
Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	Glu	Thr	Val	Glu	Tyr	Ser		
			265					270					275				
act	cac	cgc	gct	gcg	gaa	acc	gtg	ctc	aag	tac	tat	gca	cgc	cag	ctg	979	
Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
		280					285					290					
cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cgc	atg	aat	aag	gtc	1027	
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
		295				300					305						
acc	ccg	cag	ctg	ctt	gcg	ctg	gca	gat	gca	ggg	cac	aac	gac	gtg	cca	1075	
Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro		
310					315					320					325		
agc	cgc	gtg	gat	gag	cct	tat	cga	cgc	gcc	gtc	cat	ggc	gtt	cgc	gga	1123	
Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
				330					335					340			
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171	
Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu		
			345					350					355				
ggc	gtg	tgg	ttc	aag	gtc	ttt	act	cca	tac	gca	tct	ccg	gaa	gaa	ttc	1219	
Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		
		360					365					370					
tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267	
Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	Arg	Glu	Ser	Lys	Asp		

375	380	385	
ggt ctc att gcc gat gat cgt ttg tct gtg ctg att tct gcc atc gag Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu Ile Ser Ala Ile Glu 390 395 400 405			1315
agc ttt gga ttc aac ctt tac gca ctg gat ctg cgc caa aac tcc gaa Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu 410 415 420			1363
agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr 425 430 435			1411
gca aac tac cgc gag ctg tct gaa gca gag aag ctt gag gtg ctg ctg Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu 440 445 450			1459
aag gaa ctg cgc agc cct cgt ccg ctg atc ccg cac ggt tca gat gaa Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu 455 460 465			1507
tac agc gag gtc acc gac cgc gag ctc ggc atc ttc cgc acc gcg tcg Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser 470 475 480 485			1555
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile 490 495 500			1603
tcc atg gca tca tcg gtc acc gat gtg ctc gag ccg atg gtg ttg ctc Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu 505 510 515			1651
aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr 520 525 530			1699
gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly 535 540 545			1747
gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr 550 555 560 565			1795
ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp 570 575 580			1843
tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp 585 590 595			1891
gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu 600 605 610			1939
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro 615 620 625			1987

tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser 630 635 640 645	2035
gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn 650 655 660	2083
ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu 665 670 675	2131
gag gca tcg ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala 680 685 690	2179
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala 695 700 705	2227
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser 710 715 720 725	2275
acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser 730 735 740	2323
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp 745 750 755	2371
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly 760 765 770	2419
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr 775 780 785	2467
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe 790 795 800 805	2515
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu 810 815 820	2563
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala 825 830 835	2611
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys 840 845 850	2659
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro 855 860 865	2707

ctt ctc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc 2755
 Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu
 870 875 880 885

 aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa 2803
 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
 890 895 900

 agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc 2851
 Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
 905 910 915

 act gcg ctg cgc aac tcc ggc tagtccagcc ggctgggtag tac 2895
 Thr Ala Leu Arg Asn Ser Gly
 920

<210> 110

<211> 924

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Val Phe Lys Val Val Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe
 1 5 10 15

 Leu Gly Gln Ile Leu Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu
 20 25 30

 Val Tyr Glu Leu Val Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala
 35 40 45

 Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
 50 55 60

 Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
 65 70 75 80

 Leu Leu Ala Asn Leu Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu
 85 90 95

 Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
 100 105 110

 Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
 115 120 125

 Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
 130 135 140

 Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr
 145 150 155 160

 Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
 165 170 175

 Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
 180 185 190

 Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
 195 200 205

Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu
 210 215 220
 Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg
 225 230 235 240
 Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly
 245 250 255
 Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu
 260 265 270
 Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr
 275 280 285
 Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp
 290 295 300
 Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly
 305 310 315 320
 His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val
 325 330 335
 His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
 340 345 350
 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
 355 360 365
 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
 370 375 380
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
 385 390 395 400
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
 405 410 415
 Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu
 420 425 430
 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
 435 440 445
 Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro
 450 455 460
 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile
 465 470 475 480
 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val
 485 490 495
 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu
 500 505 510
 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp
 515 520 525

Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu
 530 535 540
 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp
 545 550 555 560
 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met
 565 570 575
 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
 610 615 620
 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
 625 630 635 640
 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
 645 650 655
 Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
 660 665 670
 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
 725 730 735
 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
 740 745 750
 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
 805 810 815
 Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro
 820 825 830
 Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr
 835 840 845
 Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu

850		855		860	
Leu Asp Asp Asn Pro	Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro				
865		870		875	880
Tyr Leu Leu Pro	Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr				
	885		890		895
Arg Lys Gly Asp Gln Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr					
	900		905		910
Met Asn Gly Leu Ser Thr Ala Leu Arg Asn Ser Gly					
	915		920		

<210> 111
 <211> 939
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(916)
 <223> RXN02326
 <400> 111
 ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60
 ttcgaactca tcgaagacaa ctacgcaagc cgtaaagc atg ctg gga cgc cca 115
 Met Leu Gly Arg Pro
 1 5
 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His
 10 15 20
 ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211
 Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln
 25 30 35
 aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259
 Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
 40 45 50
 ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307
 Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
 55 60 65
 gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355
 Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu
 70 75 80 85
 gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403
 Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser
 90 95 100
 ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451
 Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His
 105 110 115
 cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499

Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
 120 125 130
 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
 135 140 145
 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
 150 155 160 165
 aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
 170 175 180
 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
 185 190 195
 aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
 200 205 210
 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787
 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225
 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245
 tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Pro Ala Ala Thr Lys
 250 255 260
 gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270
 ccc 939

<210> 112

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 112

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
 1 5 10 15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr

65		70		75		80
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys						
	85			90		95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu						
	100			105		110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp						
	115			120		125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile						
	130			135		140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile						
	145			150		155
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn						
	165			170		175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val						
	180			185		190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala						
	195			200		205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu						
	210			215		220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu						
	225			230		235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val						
	245			250		255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser						
	260			265		270

<210> 113

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA02326

<400> 113

ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60

ttcgaactca tcgaagacaa ctacgcaagc cgtaaatgag atg ctg gga cgc cca	115
Met Leu Gly Arg Pro	
1 5	

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac	163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His	

10										15					20					
ctc	gtt	ggt	gcg	ggt	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa	211				
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln					
25										30					35					
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt	259				
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu					
40										45					50					
ggt	aac	cct	cca	ggt	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg	307				
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu					
55										60					65					
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa	355				
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu					
70										75					80					85
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc	403				
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser					
90										95					100					
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac	451				
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His					
105										110					115					
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc	499				
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe					
120										125					130					
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547				
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val					
135										140					145					
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595				
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp					
150										155					160					165
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca	643				
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro					
170										175					180					
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa	691				
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu					
185										190					195					
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt	739				
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly					
200										205					210					
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat	787				
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp					
215										220					225					
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835				
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala					
230										235					240					245
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883				
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys					
250										255					260					

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270

ccc

939

<210> 114

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
 1 5 10 15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 195 200 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 210 215 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 225 230 235 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
 245 250 255

Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 260 265 270

<210> 115
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXN02327

<400> 115
 accgctgaag cagcttgcc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60
 ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115
 Leu Leu Ala Thr Arg
 1 5
 gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20
 act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35
 gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50
 ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65
 cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85
 ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100
 gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115
 ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130
 gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
200 205 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
215 220 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230 235 240 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
250 255 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
265 270 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
280 285 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
295 300 305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310 315 320

caa 1083

<210> 116
<211> 320
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 116
Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
1 5 10 15
Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
20 25 30
Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
35 40 45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110
 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140
 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175
 Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190
 His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205
 Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220
 Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240
 Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255
 Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270
 Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285
 Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300
 Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 305 310 315 320

<210> 117

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> FRXA02327

<400> 117

```

accgctgaag cagcttggcc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60

ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115
                                   Leu Leu Ala Thr Arg
                                   1 5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
                                   10 15 20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
                                   25 30 35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
                                   40 45 50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
                                   55 60 65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
                                   70 75 80 85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
                                   90 95 100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
                                   105 110 115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
                                   120 125 130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
                                   135 140 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
                                   150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
                                   170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
                                   185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739

```

```

Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
    200                      205                      210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac   787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
    215                      220                      225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc   835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
    230                      235                      240                      245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg   883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
    250                      255                      260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc   931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
    265                      270                      275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag   979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
    280                      285                      290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt   1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
    295                      300                      305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
    310                      315                      320

caa                                                                    1083

```

<210> 118

<211> 320

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 118

```

Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
  1                      5                      10                      15

```

```

Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
    20                      25                      30

```

```

Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
    35                      40                      45

```

```

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
    50                      55                      60

```

```

Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
    65                      70                      75                      80

```

```

Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
    85                      90                      95

```

```

Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
    100                      105                      110

```

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 305 310 315 320

<210> 119
 <211> 1719
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1696)
 <223> RXN02328

<400> 119
 gaagtcgtgc aggtcagggg agtggtgccc gaaaacattg agaggaaaac aaaaaccgat 60

gtttgattgg gggaatcggg ggttacgata ctaggacgca gtg act gct atc acc 115
 Val Thr Ala Ile Thr
 1 5

ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163

Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr Leu Val Ser Thr His	
10 15 20	
aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc	211
Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg	
25 30 35	
ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca	259
Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala	
40 45 50	
gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc	307
Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg	
55 60 65	
tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc	355
Ser Phe Ala Ser Glu Val Arg Ile Gly Thr Glu Gly Ser Pro Val	
70 75 80 85	
aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt	403
Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val	
90 95 100	
aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc	451
Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala	
105 110 115	
cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca	499
Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro	
120 125 130	
acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc	547
Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr	
135 140 145	
gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc	595
Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser	
150 155 160 165	
aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc	643
Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro	
170 175 180	
atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt	691
Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe	
185 190 195	
gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt	739
Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg	
200 205 210	
gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct	787
Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala	
215 220 225	
gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act	835
Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr	
230 235 240 245	
gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt	883
Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg	

250							255					260					
cac	caa	aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa	931	
His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu		
			265				270						275				
ctg	cgt	gat	cgc	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cgc	tcc	att	979	
Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile		
			280				285						290				
ggt	tac	cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc	1027	
Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly		
			295				300						305				
aac	cac	gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc	1075	
Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr		
310						315						320			325		
gtg	act	gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cgc	1123	
Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg		
			330						335						340		
ttg	gct	gct	ggt	gca	acc	ttg	aag	gaa	ttg	ggt	ctg	acc	caa	gat	aag	1171	
Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys		
			345						350						355		
atc	aag	acc	cac	ggt	gca	gca	ctg	cag	tgc	cgc	atc	acc	acg	gaa	gat	1219	
Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp		
			360						365						370		
cca	aac	aac	ggc	ttc	cgc	cca	gat	acc	gga	act	atc	acc	gcg	tac	cgc	1267	
Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg		
			375			380						385					
tca	cca	ggc	gga	gct	ggc	gtt	cgt	ctt	gac	ggt	gca	gct	cag	ctc	ggt	1315	
Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly		
390						395						400			405		
ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	gtg	aaa	atg	acc	tgc	1363	
Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys		
			410						415						420		
cgt	ggt	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	gca	cag	cgc	gcg	ttg	1411	
Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu		
			425						430						435		
gct	gag	ttc	acc	gtg	tct	ggt	gtt	gca	acc	aac	att	ggt	ttc	ttg	cgt	1459	
Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg		
			440						445						450		
gcg	ttg	ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag	cgc	atc	gcc	acc	gga	1507	
Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg	Ile	Ala	Thr	Gly		
			455			460						465					
ttc	att	gcc	gat	cac	ccg	cac	ctc	ctt	cag	gct	cca	cct	gct	gat	gat	1555	
Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp		
470						475						480			485		
gag	cag	gga	cgc	atc	ctg	gat	tac	ttg	gca	gat	gtc	acc	gtg	aac	aag	1603	
Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys		
			490						495						500		

cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg 1651
 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
 505 510 515

cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc 1696
 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 520 525 530

tgaagcagct tggcccagcc gcg 1719

<210> 120

<211> 532

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Val Thr Ala Ile Thr Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr
 1 5 10 15

Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
 20 25 30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
 35 40 45

Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
 50 55 60

Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 65 70 75 80

Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
 85 90 95

Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
 100 105 110

Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
 130 135 140

Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
 180 185 190

Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
 195 200 205

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile

225 230 235 240
 Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
 245 250 255
 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
 260 265 270
 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
 275 280 285
 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
 290 295 300
 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
 305 310 315 320
 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
 325 330 335
 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
 340 345 350
 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg
 355 360 365
 Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
 370 375 380
 Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
 385 390 395 400
 Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu
 405 410 415
 Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg
 420 425 430
 Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn
 435 440 445
 Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
 450 455 460
 Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala
 465 470 475 480
 Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp
 485 490 495
 Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala
 500 505 510
 Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly
 515 520 525
 Ser Arg Asp Arg
 530

<210> 121

<211> 1406
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1383)
 <223> FRXA02328

<400> 121
 gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg 48
 Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
 1 5 10 15

tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca 96
 Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt 144
 Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca 192
 Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg 240
 Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac 288
 Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt 336
 Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct 384
 Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct 432
 Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att 480
 Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa 528
 Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa 576
 Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt 624
 Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac	672
Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr	
210 215 220	
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac	720
Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His	
225 230 235 240	
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act	768
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr	
245 250 255	
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct	816
Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala	
260 265 270	
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag	864
Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys	
275 280 285	
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac	912
Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn	
290 295 300	
aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca	960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro	
305 310 315 320	
ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa	1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu	
325 330 335	
atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt	1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly	
340 345 350	
tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag	1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu	
355 360 365	
ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg	1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu	
370 375 380	
ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att	1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile	
385 390 395 400	
gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag	1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln	
405 410 415	
gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat	1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His	
420 425 430	
ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac	1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn	
435 440 445	

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

tggcccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
 1 5 10 15

Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
 210 215 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
 225 230 235 240

Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
 245 250 255

Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
 260 265 270
 Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
 275 280 285
 Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
 290 295 300
 Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
 305 310 315 320
 Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
 325 330 335
 Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
 340 345 350
 Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
 355 360 365
 Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
 370 375 380
 Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

<210> 123

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN01048

<400> 123

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931

Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaaa cttgaggcccc aca 1347
 Pro Ile Phe

<210> 124

<211> 408

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 124

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
 370 375 380
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe

405

<210> 125
 <211> 311
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(288)
 <223> FRXA01048

<400> 125
 cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95
 taagagcaaa cttgaggccc aca 311

<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
85 90 95

```
<210> 127
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA00290
```

<400> 127																
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60																
gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115																
Met Thr Ile Asp Leu 1 5																
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163																
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His 10 15 20																
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211																
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met 25 30 35																
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259																
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu 40 45 50																
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307																
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly 55 60 65																
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355																
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly 70 75 80 85																
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403																
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln 90 95 100																
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451																
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp 105 110 115																
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499																
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro 120 125 130																
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547																
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe 135 140 145																

```

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
170 175 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
185 190 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
200 205 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
215 220 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230 235 240 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
310 315 320

```

<210> 128

<211> 321

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 128

```

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
1 5 10 15

```

```

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
20 25 30

```

```

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
35 40 45

```

```

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr

```

50 55 60
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 129
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<223> RXA02694

attaaaggtg taacaaagga atccgggcac aagctcttgc tgattttctg agctgctttg 60

agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa 739
 Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys
 200 205 210

att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225
 ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245
 gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260
 cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275
 gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290
 cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
 295 300 305
 cag aag cag ttc ttc taaatctttg gcgcctagtt ggc 1065
 Gln Lys Gln Phe Phe
 310

<210> 130

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp
 1 5 10 15
 Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp
 20 25 30
 His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45
 Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60
 Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80
 Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95
 Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110
 Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125
 Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val

194

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

```

cagtggacaa ctacttggcg ggtcttaaat cagctgtgaa ggattctgca taagctgggc 60
accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt 115
                                         Met Ile Lys Arg Leu
                                         1 5

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg 163
Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu
                        10 15 20

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt 211
Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe
                        25 30 35

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc 259
Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val
                        40 45 50

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac 307
Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His
                        55 60 65

acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg 355
Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu
                        70 75 80 85

gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca 403
Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr
                        90 95 100

ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc 451
Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile
                        105 110 115

acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag 499
Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys
                        120 125 130

aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat 547
Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr
                        135 140 145

gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta 595
Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu
                        150 155 160 165

act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca 643
Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala
                        170 175 180

gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg 691
Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met
                        185 190 195

```

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
 440 445 450
 gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc 1507
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
 455 460 465
 cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
 470 475 480 485
 gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
 490 495 500
 gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
 505 510 515
 aaa gtt ttg ccg tagcaaaaag ccggaccctt gct 1686
 Lys Val Leu Pro
 520

<210> 226

<211> 521

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
 1 5 10 15
 Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
 20 25 30
 Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45
 Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60
 Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80
 Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95
 Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110
 Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125
 Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140
 Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
 290 295 300
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
 305 310 315 320
 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
 325 330 335
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
 340 345 350
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
 355 360 365
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
 370 375 380
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
 385 390 395 400
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
 435 440 445
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
 450 455 460
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
 465 470 475 480
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

```

                485                490                495
Lys Met Pro Arg Lys Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys
                500                505                510

Leu Gly Lys Ile Phe Lys Val Leu Pro
                515                520

<210> 227
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXN02674

<400> 227
atcgacctct agggcagcag tgattgattt cataaaaatc acaagtttgt aactaaaggt 60

acagttggtg aagtatccac aatcaacttt aggagacctt gtg act gca aca ttt 115
                Val Thr Ala Thr Phe
                1                5

gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag 163
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu
                10                15                20

gga aac tcg gat cga att tcc acc aat atc aat cct tac gac gat tcc 211
Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn Pro Tyr Asp Asp Ser
                25                30                35

gta atc gcc gaa agc aaa caa gct tcc att gct gat gtt gat gcc gcg 259
Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala Asp Val Asp Ala Ala
                40                45                50

tat gaa gcc gcg aag aag gcc cag gct gag tgg gca gct acg ccc gct 307
Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp Ala Ala Thr Pro Ala
                55                60                65

gcg gaa cga tct gcc atc atc tac cgt gcg gct gaa ctt ctt gaa gag 355
Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala Glu Leu Leu Glu Glu
                70                75                80                85

cac cgg gag gaa atc gtg gaa tgg ctg atc aag gaa tcc ggc tcg acg 403
His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys Glu Ser Gly Ser Thr
                90                95                100

cgt tcc aag gct aat ttg gaa atc act ttg gca gga aac atc act aaa 451
Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala Gly Asn Ile Thr Lys
                105                110                115

gaa tcg gct tca ttc cct ggt cgt gtg cat ggt cga att tct cct tcg 499
Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly Arg Ile Ser Pro Ser
                120                125                130

aat act ccg ggc aaa gaa aac cgt gtg tac cgc gta gcc aag ggc gtt 547
Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val
                135                140                145

```

gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc	595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg	
150 155 160 165	
tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct	643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro	
170 175 180	
gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt	691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe	
185 190 195	
gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca	739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala	
200 205 210	
gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg	787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu	
215 220 225	
att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg	835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu	
230 235 240 245	
gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc	883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly	
250 255 260	
aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	

cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag 1315
 Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
 390 395 400 405

 ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag 1363
 Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys
 410 415 420

 gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg 1411
 Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met
 425 430 435

 gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc 1459
 Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
 440 445 450

 ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg 1507
 Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
 455 460 465

 atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552
 Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser
 470 475 480

 taattgtttt tcgacgtaac ccc 1575

<210> 228
 <211> 484
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 228
 Val Thr Ala Thr Phe Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly
 1 5 10 15
 Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
 20 25 30
 Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
 35 40 45
 Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
 50 55 60
 Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
 65 70 75 80
 Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
 85 90 95
 Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
 100 105 110
 Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
 115 120 125
 Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
 130 135 140
 Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu

145		150		155		160
Asn Leu Ser Ile Arg	Ser Val Ala Pro	Ala Leu Ala Val Gly	Asn Ala			
	165		170			175
Val Val Ile Lys Pro	Ala Ser Asp Thr	Pro Val Thr Gly	Gly Val Ile			
	180		185			190
Pro Ala Arg Ile Phe	Glu Glu Ala Gly	Val Pro Ala Gly	Val Ile Ser			
	195		200			205
Thr Val Ala Gly Ala	Gly Ser Glu Ile Gly	Asp His Phe Val Thr	His			
	210		215			220
Ala Val Pro Lys Leu	Ile Ser Phe Thr Gly	Ser Thr Pro Val Gly	Arg			
	225		230			240
Arg Val Gly Glu Leu	Ala Ile Asn Gly Gly	Pro Met Lys Thr Val	Ala			
	245		250			255
Leu Glu Leu Gly Gly	Asn Ala Pro Phe Val	Val Leu Ala Asp	Ala Asp			
	260		265			270
Ile Asp Ala Ala Ala	Gln Ala Ala Ala Val	Gly Ala Phe Leu His	Gln			
	275		280			285
Gly Gln Ile Cys Met	Ser Ile Asn Arg Val Ile	Val Asp Ala Ala Val				
	290		295			300
His Asp Glu Phe Leu	Glu Lys Phe Val Glu	Ala Val Lys Asn Ile Pro				
	305		310			320
Thr Gly Asp Pro Ser	Ala Glu Gly Thr Leu	Val Gly Pro Val Ile	Asn			
	325		330			335
Asp Ser Gln Leu Ser	Gly Leu Lys Glu Lys	Ile Glu Leu Ala Lys	Lys			
	340		345			350
Glu Gly Ala Thr Val	Gln Val Glu Gly Pro	Ile Glu Gly Arg Leu	Val			
	355		360			365
His Pro His Val Phe	Ser Asp Val Thr Ser	Asp Met Glu Ile Ala	Arg			
	370		375			380
Glu Glu Ile Phe Gly	Pro Leu Ile Ser Val	Leu Lys Ala Asp Asp	Glu			
	385		390			400
Ala His Ala Ala Glu	Leu Ala Asn Ala Ser	Asp Phe Gly Leu Ser	Ala			
	405		410			415
Ala Val Trp Ser Lys	Asp Ile Asp Arg Ala	Ala Gln Phe Ala Leu	Gln			
	420		425			430
Ile Asp Ser Gly Met	Val His Ile Asn Asp	Leu Thr Val Asn Asp	Glu			
	435		440			445
Pro His Val Met Phe	Gly Gly Ser Lys Asn	Ser Gly Leu Gly Arg	Phe			
	450		455			460
Asn Gly Asp Trp Ala	Ile Glu Glu Phe Thr	Thr Asp Arg Trp Ile	Gly			
	465		470			480

Ile Lys Arg Ser

<210> 229

<211> 2034

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2011)

<223> RXN00868

<400> 229

```

cgatgaccca gcgcacgcct gggttcgaga tacatggacc gggcaagcat ttgatgatcg 60
cttgccatat gagaacgcaa acaaggagggg ataaaatttc atg gct gaa acg aag 115
                                         Met Ala Glu Thr Lys
                                         1 5

aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg 163
Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp
                        10 15 20

act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga 211
Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly
                        25 30 35

att ttc gga cac gga aac gtt gct ggc att ggc cag gca ctc aag cag 259
Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly Gln Ala Leu Lys Gln
                        40 45 50

tac aac gtt gaa caa cct gag ctc atg ccg tac tac cag gct cgt aat 307
Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr Tyr Gln Ala Arg Asn
                        55 60 65

gag cag gcg atg gtg cac cag tct gtt gga tat gca cgc atg cac cgc 355
Glu Gln Ala Met Val His Gln Ser Val Gly Tyr Ala Arg Met His Arg
                        70 75 80 85

cgt cgt ggc aca tac gca tct gcc gca tct gtt gga ccc ggc gcg acc 403
Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val Gly Pro Gly Ala Thr
                        90 95 100

aac ctg tta acc ggt gcg gct ctt gct acc acc aac cgt ttg cca gcg 451
Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr Asn Arg Leu Pro Ala
                        105 110 115

ttg ctg ctg cct agt gat act ttt gcc acc cgc gtg gcg gat cca gtg 499
Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg Val Ala Asp Pro Val
                        120 125 130

ttg cag cag ttg gag cag cca tgg gat atc ggg ctg acg gtt aat gat 547
Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly Leu Thr Val Asn Asp
                        135 140 145

gct ttc cgc cct gtg tct aag ttc ttt gat cgg gtg cag cgc ccg gag 595
Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg Val Gln Arg Pro Glu
150 155 160 165

```

cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc	643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro	
170 175 180	
gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct	691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala	
185 190 195	
gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac	739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His	
200 205 210	
att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa	787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu	
215 220 225	
gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg	835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
230 235 240 245	
ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act	883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr	
250 255 260	
ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg	931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp	
265 270 275	
gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct	979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala	
280 285 290	
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act	1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr	
295 300 305	
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct	1075
Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro	
310 315 320 325	
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag	1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
330 335 340	
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg	1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
345 350 355	
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg	1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala	
360 365 370	
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag	1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys	
375 380 385	
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc	1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile	
390 395 400 405	

ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc	1363
Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala	
410 415 420	
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat	1411
Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp	
425 430 435	
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa	1459
Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu	
440 445 450	
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat	1507
Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp	
455 460 465	
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc	1555
Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu	
470 475 480 485	
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg	1603
Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val	
490 495 500	
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa	1651
Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu	
505 510 515	
act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct	1699
Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala	
520 525 530	
gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg	1747
Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala	
535 540 545	
atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc	1795
Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser	
550 555 560 565	
gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct	1843
Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala	
570 575 580	
tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac	1891
Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr	
585 590 595	
gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc	1939
Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser	
600 605 610	
act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa	1987
Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln	
615 620 625	
gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa	2034
Ala Leu Gln Arg Pro Leu Leu Gly	
630 635	

<210> 230
 <211> 637
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230

Met	Ala	Glu	Thr	Lys	Arg	Met	Thr	Val	Ser	Gln	Ala	Leu	Val	Glu	Phe
1				5					10					15	
Leu	Gly	His	Gln	Trp	Thr	Val	Asp	Gly	Asp	Ile	Arg	Glu	Arg	Thr	Ile
			20					25					30		
Pro	Gly	Met	Phe	Gly	Ile	Phe	Gly	His	Gly	Asn	Val	Ala	Gly	Ile	Gly
		35					40					45			
Gln	Ala	Leu	Lys	Gln	Tyr	Asn	Val	Glu	Gln	Pro	Glu	Leu	Met	Pro	Tyr
		50				55					60				
Tyr	Gln	Ala	Arg	Asn	Glu	Gln	Ala	Met	Val	His	Gln	Ser	Val	Gly	Tyr
	65				70					75					80
Ala	Arg	Met	His	Arg	Arg	Arg	Gly	Thr	Tyr	Ala	Ser	Ala	Ala	Ser	Val
				85					90					95	
Gly	Pro	Gly	Ala	Thr	Asn	Leu	Leu	Thr	Gly	Ala	Ala	Leu	Ala	Thr	Thr
			100					105					110		
Asn	Arg	Leu	Pro	Ala	Leu	Leu	Leu	Pro	Ser	Asp	Thr	Phe	Ala	Thr	Arg
		115					120					125			
Val	Ala	Asp	Pro	Val	Leu	Gln	Gln	Leu	Glu	Gln	Pro	Trp	Asp	Ile	Gly
		130				135					140				
Leu	Thr	Val	Asn	Asp	Ala	Phe	Arg	Pro	Val	Ser	Lys	Phe	Phe	Asp	Arg
	145				150					155					160
Val	Gln	Arg	Pro	Glu	Gln	Leu	Phe	Ser	Ile	Ala	Leu	Ala	Ala	Met	Arg
			165					170						175	
Val	Leu	Thr	Asp	Pro	Ala	Glu	Thr	Gly	Ala	Val	Thr	Ile	Ala	Leu	Pro
		180						185					190		
Glu	Asp	Val	Gln	Ala	Glu	Met	Leu	Asp	Val	Pro	Val	Glu	Phe	Leu	Gln
		195					200					205			
Asp	Arg	Glu	Trp	His	Ile	Arg	Arg	Pro	Arg	Pro	Glu	Arg	Ala	Ala	Leu
		210				215					220				
Ala	Arg	Ala	Ile	Glu	Val	Ile	Lys	Asn	Ala	Lys	Asn	Pro	Met	Ile	Ile
	225				230					235					240
Ala	Gly	Gly	Gly	Val	Leu	Tyr	Ser	Asp	Ala	Glu	Thr	Gln	Leu	Gln	Ala
			245					250						255	
Leu	Val	Glu	Gln	Thr	Gly	Ile	Pro	Val	Gly	Thr	Ser	Gln	Ala	Gly	Gly
		260						265					270		
Gly	Val	Leu	Ala	Trp	Asp	His	Ala	Gln	Asn	Leu	Gly	Gly	Val	Gly	Ala
		275					280					285			
Thr	Gly	Thr	Leu	Ala	Ala	Asn	Arg	Ile	Ala	Gly	Asp	Ala	Asp	Val	Ile

290	295	300
Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr 305 310 315 320		
Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser 325 330 335		
Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala 340 345 350		
Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val 355 360 365		
Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp 370 375 380		
Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly 385 390 395 400		
Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp 405 410 415		
Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu 420 425 430		
Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser 435 440 445		
Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu 450 455 460		
Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly 465 470 475 480		
Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly 485 490 495		
Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile 500 505 510		
Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr 515 520 525		
Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu 530 535 540		
Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile 545 550 555 560		
Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met 565 570 575		
Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser 580 585 590		
Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro 595 600 605		
Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp 610 615 620		

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
625 630 635

<210> 231
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1119)
<223> RXN01143

<400> 231
atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct 48
Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
1 5 10 15
cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96
His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
20 25 30
gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144
Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
35 40 45
ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
50 55 60
aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag 240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
65 70 75 80
cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
85 90 95
ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
100 105 110
gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
115 120 125
tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
130 135 140
acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
145 150 155 160
ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
165 170 175
cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt 576

Arg	Thr	Trp	Leu	Asn	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Ala	Val		
			180					185					190				
cct	gcg	gcc	ctt	gga	gca	aag	gct	ggc	gca	cct	gac	aag	gaa	gtc	tg	624	
Pro	Ala	Ala	Leu	Gly	Ala	Lys	Ala	Gly	Ala	Pro	Asp	Lys	Glu	Val	Trp		
		195					200					205					
gct	atc	gac	ggc	gac	ggc	tgt	ttc	cag	atg	acc	aac	cag	gaa	ctc	acc	672	
Ala	Ile	Asp	Gly	Asp	Gly	Cys	Phe	Gln	Met	Thr	Asn	Gln	Glu	Leu	Thr		
	210					215					220						
acc	gcc	gca	gtt	gaa	ggt	ttc	ccc	att	aag	atc	gca	cta	atc	aac	aac	720	
Thr	Ala	Ala	Val	Glu	Gly	Phe	Pro	Ile	Lys	Ile	Ala	Leu	Ile	Asn	Asn		
225					230					235					240		
gga	aaa	cct	ggg	gca	tg	gtt	cgc	caa	tg	cag	acc	cta	ttc	tat	gaa	768	
Gly	Lys	Pro	Gly	Ala	Trp	Val	Arg	Gln	Trp	Gln	Thr	Leu	Phe	Tyr	Glu		
				245					250					255			
gga	cgg	tac	tca	aat	act	aaa	ctt	cgt	aac	cag	ggc	gag	tac	atg	ccc	816	
Gly	Arg	Tyr	Ser	Asn	Thr	Lys	Leu	Arg	Asn	Gln	Gly	Glu	Tyr	Met	Pro		
			260					265					270				
gac	ttt	gtt	acc	ctt	tct	gag	gga	ctt	ggc	tgt	gtt	gcc	atc	cgc	gtc	864	
Asp	Phe	Val	Thr	Leu	Ser	Glu	Gly	Leu	Gly	Cys	Val	Ala	Ile	Arg	Val		
		275					280					285					
acc	aaa	gcg	gag	gaa	gta	ctg	cca	gcc	atc	caa	aag	gct	cga	gag	atc	912	
Thr	Lys	Ala	Glu	Glu	Val	Leu	Pro	Ala	Ile	Gln	Lys	Ala	Arg	Glu	Ile		
	290					295					300						
aac	gac	cgc	cca	gta	gtc	atc	gac	ttc	atc	gtc	ggg	gaa	gac	gca	cag	960	
Asn	Asp	Arg	Pro	Val	Val	Ile	Asp	Phe	Ile	Val	Gly	Glu	Asp	Ala	Gln		
305					310					315					320		
gta	tg	cca	atg	gtg	tct	gct	gga	tca	tcc	aac	tcc	gat	atc	cag	tac	1008	
Val	Trp	Pro	Met	Val	Ser	Ala	Gly	Ser	Ser	Asn	Ser	Asp	Ile	Gln	Tyr		
				325					330					335			
gca	ctc	gga	ttg	cgc	cca	ttc	ttt	gat	ggg	gat	gaa	tct	gca	gca	gaa	1056	
Ala	Leu	Gly	Leu	Arg	Pro	Phe	Phe	Asp	Gly	Asp	Glu	Ser	Ala	Ala	Glu		
			340					345					350				
gat	cct	gcc	gac	att	cac	gaa	gcc	gtc	agc	gac	att	gat	gcc	gcc	gtt	1104	
Asp	Pro	Ala	Asp	Ile	His	Glu	Ala	Val	Ser	Asp	Ile	Asp	Ala	Ala	Val		
		355					360					365					
gaa	tcg	acc	gag	gca	taaggagaga	cccaagatgg	cta									1142	
Glu	Ser	Thr	Glu	Ala													
		370															

<210> 232

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Ile	Pro	Val	Val	Thr	Thr	Leu	Met	Ala	Leu	Gly	Thr	Phe	Pro	Glu	Ser
1				5					10					15	

His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

```

                340                345                350
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
      355                360                365

Glu Ser Thr Glu Ala
      370

<210> 233
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01146

<400> 233
tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccactcccgc 60

cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag 115
                Met Thr Gly Ala Lys
                1                5

gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
                10                15                20

att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
                25                30                35

aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
                40                45                50

gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
                55                60                65

gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
                70                75                80                85

gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
                90                95                100

agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
                105                110                115

atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac 499
Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
                120                125                130

gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
                135                140                145

```

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165

 gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180

 cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
 185 190 195

 atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
 200 205 210

 aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
 215 220 225

 atc cca 793
 Ile Pro
 230

<210> 234

<211> 231

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala
 1 5 10 15

 Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp
 20 25 30

 Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
 35 40 45

 Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60

 Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80

 Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95

 Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110

 Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
 115 120 125

 Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
 130 135 140

 Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
 145 150 155 160

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
 165 170 175

Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
 180 185 190

Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
 195 200 205

Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
 210 215 220

Ala Glu Tyr Thr Gly Ile Pro
 225 230

<210> 235

<211> 639

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(616)

<223> RXN01144

<400> 235

ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60

gccgccgttg aatcgaccga ggcataagga gagaccaag atg gct aat tct gac 115
 Met Ala Asn Ser Asp
 1 5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
 10 15 20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
 25 30 35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
 Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
 40 45 50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
 55 60 65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
 70 75 80 85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
 90 95 100

acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
 Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
 105 110 115

```

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
      120                125                130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
      135                140                145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
      150                155                160                165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
Thr Met Ala Pro Ala Lys Ile
      170

```

<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

```

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
  1              5              10              15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
      20                25                30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
      35                40                45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
      50                55                60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
      65                70                75                80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
      85                90                95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
      100               105               110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
      115               120               125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
      130               135               140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
      145               150               155               160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
      165               170

```

<210> 237

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

```

tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60
aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
                               Met Ser Lys Val Ala
                               1 5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
                               10 15 20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
                               25 30 35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
                               40 45 50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
                               55 60 65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
                               70 75 80 85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc 403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
                               90 95 100

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt 451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
                               105 110 115

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa 499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
                               120 125 130

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
                               135 140 145

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
                               150 155 160 165

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc 643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
                               170 175 180

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc 691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
                               185 190 195

```


Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 239
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXA02453

<400> 239
 aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
 Met Lys Ser Ile Phe
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
 Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130
 tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145
 gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165
 cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180
 ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195
 gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210
 tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225
 ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245
 gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 240

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
 1 5 10 15
 Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30
 Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45
 Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60
 Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80
 Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 241

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXS01758

<400> 241

cccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60

gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile 5
 1

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val 20
 10 15

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala 35
 25 30

agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys 50
 40 45

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027

Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305
 gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325
 gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335
 taatgccaac agcaagccca att 1140

<210> 242
 <211> 339
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 242
 Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
 1 5 10 15
 Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
 20 25 30
 Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45
 Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60
 Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80
 Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95
 Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110
 Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125
 Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140
 Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160
 Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175
 Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190
 Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205
 Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
 260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 243

<211> 1665

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1642)

<223> RXA02737

<400> 243

agcagctgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccggt 60

acacatcttt cattaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
 Val Ser Thr Asn Thr
 1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
 10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
 Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
 25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
 Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
 40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
 Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
 55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

70	75	80	85	
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc				403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu	90	95	100	
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct				451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala	105	110	115	
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc				499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly	120	125	130	
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc				547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe	135	140	145	
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc				595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr	150	155	160	165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac				643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn	170	175	180	
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca				691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro	185	190	195	
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt				739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val	200	205	210	
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg				787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu	215	220	225	
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat				835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp	230	235	240	245
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc				883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala	250	255	260	
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc				931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala	265	270	275	
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag				979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys	280	285	290	
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc				1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr	295	300	305	
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc				1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val	310	315	320	325

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag 1123
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu
330 335 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt 1171
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
440 445 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
455 460 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
505 510

gcaaaaaatg atc 1665

<210> 244

<211> 514

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp
1 5 10 15

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val
 20 25 30
 Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
 50 55 60
 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
 290 295 300
 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320
 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

340 345 350
 Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
 355 360 365
 Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His
 370 375 380
 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile
 385 390 395 400
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
 405 410 415
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
 420 425 430
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
 465 470 475 480
 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
 485 490 495
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
 500 505 510
 Arg Pro

<210> 245
 <211> 1203
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1180)
 <223> RXA02738

<400> 245
 ttgttgtaa tcggtacaaa gggctttaag cacatccctt acttgcctgc tctccttgag 60
 cacagttcaa gaacaattct ttaaggaaa atttagtttc atg tct cac att gat 115
 Met Ser His Ile Asp
 1 5
 gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
 10 15 20
 gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
 25 30 35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc	259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser	
40 45 50	
aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc	307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
55 60 65	
gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc	355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
70 75 80 85	
aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac	403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
90 95 100	
gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc	451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
105 110 115	
gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt	499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
120 125 130	
cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca	547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc	595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
150 155 160 165	
ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc	643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct	691
Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
185 190 195	
gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc	739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
200 205 210	
ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca	787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala	
215 220 225	
ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc	835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe	
230 235 240 245	
gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg	883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
250 255 260	
gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt	931
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc	979

Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
 280 285 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
 310 315 320 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala
 345 350 355

cgc ctg aag tagaatcagc acgctgcac agt 1203
 Arg Leu Lys
 360

<210> 246

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
 1 5 10 15

Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
 20 25 30

Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
 35 40 45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60

Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80

Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 100 105 110

Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
 130 135 140

Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 145 150 155 160

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala

```

                165                170                175
Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
      180                185                190
Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
      195                200                205
Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
      210                215                220
Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
      225                230                235                240
Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
      245                250                255
Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
      260                265                270
Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
      275                280                285
Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His
      290                295                300
Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
      305                310                315                320
Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
      325                330                335
Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
      340                345                350
Glu Ser Met Glu Ala Arg Leu Lys
      355                360

<210> 247
<211> 2223
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2200)
<223> RXA02739

<400> 247
cctttgccaa atttgaacca attaacctaa gtcgtagatc tgatcatcgg atctaacgaa 60

aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg 115
                        Leu Thr Thr Leu Thr
                        1                    5

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163
Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp
      10                15                20

tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct 211

```

Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala		
			25					30					35				
gca	gac	gct	gta	gaa	aac	tgt	ggc	tcc	ggc	cac	cca	ggc	acc	gca	atg	259	
Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met		
		40					45					50					
agc	ctg	gct	ccc	ctt	gca	tac	acc	ttg	tac	cag	cgg	gtt	atg	aac	gta	307	
Ser	Leu	Ala	Pro	Leu	Ala	Tyr	Thr	Leu	Tyr	Gln	Arg	Val	Met	Asn	Val		
	55					60					65						
gat	cca	cag	gac	acc	aac	tgg	gca	ggc	cgt	gac	cgc	ttc	gtt	ctt	tct	355	
Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser		
70					75					80					85		
tgt	ggc	cac	tcc	tct	ttg	acc	cag	tac	atc	cag	ctt	tac	ttg	ggg	gga	403	
Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly		
				90					95					100			
ttc	ggc	ctt	gag	atg	gat	gac	ctg	aag	gct	ctg	cgc	acc	tgg	gat	tcc	451	
Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser		
			105					110					115				
ttg	acc	cca	gga	cac	cct	gag	tac	cgc	cac	acc	aag	ggc	gtt	gag	atc	499	
Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile		
		120					125					130					
acc	act	ggc	cct	ctt	ggc	cag	ggg	ctt	gca	tct	gca	gtt	ggg	atg	gcc	547	
Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala		
		135				140					145						
atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595	
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu		
150					155					160					165		
ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggg	643	
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly		
				170					175					180			
gac	ctg	cag	gaa	ggg	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691	
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr		
			185					190					195				
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739	
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser		
		200					205					210					
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787	
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg		
		215				220					225						
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835	
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp		
230					235					240					245		
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883	
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys		
				250					255					260			
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931	
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro		

265	270	275	
act atg atg aac acc ggt gct gtg cac ggt gct gct ctt ggc gca gct			979
Thr Met Met Asn Thr Gly Ala Val His Gly Ala Ala Leu Gly Ala Ala			
280	285	290	
gag gtt gca gca acc aag act gag ctt gga ttc gat cct gag gct cac			1027
Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe Asp Pro Glu Ala His			
295	300	305	
ttc gcg atc gac gat gag gtt atc gct cac acc cgc tcc ctc gca gag			1075
Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr Arg Ser Leu Ala Glu			
310	315	320	325
cgc gct gca cag aag aag gct gca tgg cag gtc aag ttc gat gag tgg			1123
Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val Lys Phe Asp Glu Trp			
330	335	340	
gca gct gcc aac cct gag aac aag gct ctg ttc gat cgc ctg aac tcc			1171
Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe Asp Arg Leu Asn Ser			
345	350	355	
cgt gag ctt cca gcg ggc tac gct gac gag ctc cca aca tgg gat gca			1219
Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu Pro Thr Trp Asp Ala			
360	365	370	
gat gag aag ggc gtc gca act cgt aag gct tcc gag gct gca ctt cag			1267
Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser Glu Ala Ala Leu Gln			
375	380	385	
gca ctg ggc aag acc ctt cct gag ctg tgg ggc ggt tcc gct gac ctc			1315
Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu			
390	395	400	405
gca ggt tcc aac aac acc gtg atc aag ggc tcc cct tcc ttc ggc cct			1363
Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser Pro Ser Phe Gly Pro			
410	415	420	
gag tcc atc tcc acc gag acc tgg tct gct gag cct tac ggc cgt aac			1411
Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu Pro Tyr Gly Arg Asn			
425	430	435	
ctg cac ttc ggt atc cgt gag cac gct atg gga tcc atc ctc aac ggc			1459
Leu His Phe Gly Ile Arg Glu His Ala Met Gly Ser Ile Leu Asn Gly			
440	445	450	
att tcc ctc cac ggt ggc acc cgc cca tac ggc gga acc ttc ctc atc			1507
Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly Gly Thr Phe Leu Ile			
455	460	465	
ttc tcc gac tac atg cgt cct gca gtt cgt ctt gca gct ctc atg gag			1555
Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu Ala Ala Leu Met Glu			
470	475	480	485
acc gac gct tac tac gtc tgg acc cac gac tcc atc ggt ctg ggc gaa			1603
Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser Ile Gly Leu Gly Glu			
490	495	500	
gat ggc cca acc cac cag cct gtt gaa acc ttg gct gca ctg cgc gcc			1651
Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu Ala Ala Leu Arg Ala			
505	510	515	

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
 600 605 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca 1987
 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
 615 620 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223
 Ala Lys Asp Ser Ile Asn Gly
 695 700

<210> 248

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg
 1 5 10 15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
 35 40 45
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
 50 55 60
 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
 195 200 205
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
 355 360 365
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
 500 505 510
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
 660 665 670
 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

675	680	685	
Ala Val Val Ala Ala Ala	Lys Asp Ser Ile Asn Gly		
690	695	700	
<210> 249			
<211> 793			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (48)..(770)			
<223> RXA00965			
<400> 249			
agattgcggg cctcggcttc attgaaaaca agacggtgtt tgaataaatg aca act	56		
	Met Thr Thr		
	1		
ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc	104		
Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly			
5 10 15			
aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc	152		
Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe			
20 25 30 35			
ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc	200		
Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala			
40 45 50			
cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca	248		
His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala			
55 60 65			
aat act ggt gag gaa acc cca atg tac gtg tcg cca gaa gcg cgc aac	296		
Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn			
70 75 80			
gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac	344		
Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn			
85 90 95			
ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg	392		
Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr			
100 105 110 115			
tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act	440		
Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr			
120 125 130			
gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc	488		
Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile			
135 140 145			
cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag	536		
His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu			
150 155 160			

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175
 caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195
 cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210
 ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225
 act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
 230 235 240
 tagtttccac acattcttaa atg 793

<210> 250

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala
 1 5 10 15
 Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
 20 25 30
 Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45
 Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60
 His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80
 Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95
 Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110
 Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125
 Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140
 Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160
 Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
 210 215 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
 225 230 235 240

Leu

<210> 251
 <211> 1575
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1552)
 <223> RXN00999

<400> 251
 cctcctgtga cctggtataaa tcgccactac ccccaaattgg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc	499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser	
120 125 130	
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
 360 365 370

 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
 470 475 480

 taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15

 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
 465 470 475 480

Glu Val Glu Ala

<210> 253
 <211> 1537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1537)
 <223> FRXA00999

<400> 253
 cctcctgtga cctggtaaaa tcgccactac ccccaaattgg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctg gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
 120 125 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc	1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys	
360 365 370	

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc gcc gac cgc 1537
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 470 475

<210> 254

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15

 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 465 470 475

<210> 255
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02596

<400> 255
 aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60
 gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35
 cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50
 acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65
 aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85
 tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100
 ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115
 cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130
 tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145
 cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
ggt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac	979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His	
280 285 290	
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat	1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp	
295 300 305	
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat	1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp	
310 315 320 325	
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag	1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys	
330 335 340	
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg	1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu	
345 350 355	
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct	1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala	
360 365 370	
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt	1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe	
375 380 385	
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag	1313
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His	
390 395 400	
ggcatctccc aca	1326

<210> 256

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
 1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
 260 265 270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
 275 280 285

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
 385 390 395 400
 His

<210> 257
 <211> 512
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(489)
 <223> FRXA02596

<400> 257
 cct gtg gtc tac acc ggc cca ctc gac ctc tac ttc aac tac gca gag 48
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15
 ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa 96
 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30
 acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45
 gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60
 gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240
 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80
 cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca 288
 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 cgc gga cac taaaaggaag ggcatctccc aca 512
 Arg Gly His

<210> 258

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 258

Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15

 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 Arg Gly His

```
<210> 259
<211> 598
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(598)
<223> FRXA02642
```

<400> 259																
aaggtatctg	ggtgtggata	tgccctgcta	actggagaaa	cttggcccga	tcgggtgtct	60										
gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115																
Met Thr Glu Ser Lys 1 5																
aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163																
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val 10 15 20																
gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211																
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu 25 30 35																
cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259																
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu 40 45 50																
acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307																
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser 55 60 65																
aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355																
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly 70 75 80 85																
tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403																
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe 90 95 100																
ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451																
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser 105 110 115																
cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499																
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp 120 125 130																
tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547																
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly 135 140 145																
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595																
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp 150 155 160 165																
cag 598																
Gln																

<210> 260
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 260
 Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
 1 5 10 15
 Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30
 Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln
 165

<210> 261
 <211> 668
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(645)
 <223> RXA02572

<400> 261
 gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48
 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15
 gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
 35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
 50 55 60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336
 Thr Val Leu Gly Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668
 Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15

Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala

35					40					45						
Phe	Met	Ala	Arg	Ala	Gly	Glu	Leu	Gly	Ala	Asp	Gln	Ala	Leu	Thr	Phe	
50					55					60						
Leu	Arg	Glu	Val	Asp	Ser	Ile	Asn	Met	Arg	Arg	Arg	Asp	Arg	Val	Val	
65					70					75					80	
Gln	Leu	Ala	Lys	Glu	Met	Cys	Gly	Gly	Ser	Leu	Leu	Gly	Lys	Arg	Val	
85					90					95						
Thr	Val	Leu	Gly	Ala	Ala	Phe	Lys	Pro	Asn	Ser	Asp	Asp	Val	Arg	Asp	
100					105					110						
Ser	Pro	Ala	Leu	Ser	Val	Ala	Gly	Ser	Leu	Ser	Leu	Gln	Gly	Ala	Ala	
115					120					125						
Val	Ser	Val	Tyr	Asp	Pro	Glu	Ala	Met	Asp	Asn	Ala	Arg	Arg	Val	Phe	
130					135					140						
Pro	Thr	Leu	Ser	Tyr	Ala	Ser	Ser	Thr	Lys	Glu	Ala	Leu	Ile	Asp	Ala	
145					150					155					160	
His	Leu	Val	Val	Leu	Ala	Thr	Glu	Trp	Gln	Glu	Phe	Arg	Asp	Leu	Asp	
165					170					175						
Pro	Glu	Val	Ala	Gly	Gly	Val	Val	Glu	Lys	Arg	Ala	Ile	Ile	Asp	Gly	
180					185					190						
Arg	Asn	Val	Leu	Asp	Val	Ala	Lys	Trp	Lys	Ala	Ala	Gly	Trp	Glu	Met	
195					200					205						
Glu	Ala	Leu	Gly	Arg	Asn	Leu										
210					215											

<210> 263

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXA02485

<400> 263

cggtggtcag tgcttggtgc accttgccga cgggctgatt gatcgtaatg gtgttttctg 60

tacgcgttgc	catgaggata	agactaccgt	tagtggggtg	ttg	gat	tca	tcg	cta	115
					Leu	Asp	Ser	Ser	Leu
					1			5	

gcc	cag	gaa	atc	gcc	gcg	atc	gac	ggc	gtc	gaa	ctc	gat	tcg	gaa	gtc	163
Ala	Gln	Glu	Ile	Ala	Ala	Ile	Asp	Gly	Val	Glu	Leu	Asp	Ser	Glu	Val	
			10						15					20		

act	ttc	gcc	gat	ctg	acg	acc	ctc	cgc	atc	ggc	gga	aaa	ccc	cgc	agc	211
Thr	Phe	Ala	Asp	Leu	Thr	Thr	Leu	Arg	Ile	Gly	Gly	Lys	Pro	Arg	Ser	
			25					30					35			

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
40 45 50	
ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

<210> 264
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
 Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
 1 5 10 15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
 20 25 30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
 325 330 335
 Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
 340 345 350
 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 355 360 365

<210> 265

<211> 1124

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1101)

<223> RXA01216

<400> 265

acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca 48
 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
 1 5 10 15

acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
 20 25 30

ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu		
		35					40					45					
caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192	
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser		
	50					55				60							
ggt	gtc	ttt	gct	ttc	gac	gcc	gcc	atc	ttg	cgt	tcc	gca	ctg	gct	gaa	240	
Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu		
65					70				75					80			
ctg	aag	tcc	gac	aac	gct	cag	ggc	gag	ctg	tac	ctg	acc	gac	gtt	ttg	288	
Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu		
				85					90					95			
ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336	
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala		
		100						105					110				
gat	gct	cgt	gaa	ctc	gcc	ggc	gtc	aac	gat	cgt	gtg	cag	ctc	gca	gaa	384	
Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu		
		115					120					125					
gcc	ggc	gcc	gaa	cta	aac	cgt	cgc	acc	gtc	atc	gcc	gct	atg	cgt	ggt	432	
Ala	Gly	Ala	Glu	Leu	Asn	Arg	Arg	Thr	Val	Ile	Ala	Ala	Met	Arg	Gly		
	130					135					140						
ggc	gca	acc	atc	gtt	gat	cca	gca	acc	acc	tgg	atc	gat	gtg	gag	gtt	480	
Gly	Ala	Thr	Ile	Val	Asp	Pro	Ala	Thr	Thr	Trp	Ile	Asp	Val	Glu	Val		
145					150					155				160			
tct	atc	gga	cgc	gac	gtg	atc	atc	cac	cct	ggc	acc	cag	ctc	aag	ggc	528	
Ser	Ile	Gly	Arg	Asp	Val	Ile	Ile	His	Pro	Gly	Thr	Gln	Leu	Lys	Gly		
				165					170					175			
gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggt	cca	gac	acc	acc	ttg	576	
Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu		
		180						185					190				
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624	
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly		
		195					200					205					
ttc	gac	tcc	acc	atc	ggt	gaa	aac	gcc	acc	gtt	ggc	ccc	ttc	acc	tac	672	
Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr		
	210					215					220						
atc	cgc	cca	gga	acc	aca	ctg	gga	cca	gaa	ggc	aag	ctc	ggt	ggc	ttc	720	
Ile	Arg	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Glu	Gly	Lys	Leu	Gly	Gly	Phe		
225					230					235				240			
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768	
Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His		
				245					250					255			
ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816	
Leu	Thr	Tyr	Val	Gly	Asp	Ala	Thr	Ile	Gly	Glu	Glu	Ser	Asn	Ile	Gly		
			260					265					270				
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggt	gaa	aac	aag	cac	cac	acc	864	
Ala	Ser	Ser	Val	Phe	Val	Asn	Tyr	Asp	Gly	Glu	Asn	Lys	His	His	Thr		

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct			912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala			
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124
<210> 266			
<211> 367			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 266			
Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro			
1	5	10	15
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr			
	20	25	30
Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu			
	35	40	45
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser			
	50	55	60
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu			
	65	70	75
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu			
	85	90	95
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala			
	100	105	110
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu			
	115	120	125
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly			
	130	135	140
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val			
	145	150	155
			160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175
 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190
 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205
 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220
 Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240
 Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255
 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270
 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285
 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300
 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
 305 310 315 320
 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
 325 330 335
 Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
 340 345 350
 Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
 355 360 365

<210> 267

<211> 981

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> RXA01259

<400> 267

aagagaatta tttctaaaat tcggtatcgt ctaagaaatg agtttgccaa tagctcagca 60

tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115
 Met Gly Thr Arg Phe
 1 5

ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
 10 15 20

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca	211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala	
25 30 35	
act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa	259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys	
40 45 50	
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt	307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly	
55 60 65	
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca	355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala	
70 75 80 85	
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt	403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val	
90 95 100	
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc	451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val	
105 110 115	
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg	499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met	
120 125 130	
gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag	547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu	
135 140 145	
gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa	595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu	
150 155 160 165	
ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg	643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met	
170 175 180	
gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg	691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr	
185 190 195	
ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att	739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile	
200 205 210	
gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta	787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu	
215 220 225	
ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag	835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys	
230 235 240 245	
cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac	883
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr	
250 255 260	
ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg	931

Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
 1 5 10 15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
245 250 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
260 265 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
275 280 285

<210> 269

<211> 526

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA02028

<400> 269

tgcgcagttc ctgcttagtt tggctcataa atctaaggat aaccgttatt ttcggagggg 60

tacgacgatt ggggttgcg gggcaggtac tcttggttcc atg agt ttg cct atc 115
Met Ser Leu Pro Ile
1 5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163
Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
10 15 20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
25 30 35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
40 45 50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
55 60 65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
70 75 80 85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
90 95 100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
105 110 115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
120 125 130

gat gtc gta gcg gtg atg ttg ccg cac 526
Asp Val Val Ala Val Met Leu Pro His

135

140

<210> 270
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
 1 5 10 15
 Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
 20 25 30
 Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
 35 40 45
 Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
 50 55 60
 Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65 70 75 80
 Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
 85 90 95
 Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
 100 105 110
 Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
 115 120 125
 Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
 130 135 140

<210> 271
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1261)
 <223> RXA01262

<400> 271
 tatactcgtc aagggccttc gataaaacaa agacaatttt ccccgacgg gacaatctga 60
 aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
 Met Lys Ile Ala Val
 1 5
 gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
 10 15 20
 aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
 25 30 35

gtt	caa	gaa	ttt	cgt	tcg	cca	att	gtc	gat	agc	gat	ctc	gaa	gaa	tat	259
Val	Gln	Glu	Phe	Arg	Ser	Pro	Ile	Val	Asp	Ser	Asp	Leu	Glu	Glu	Tyr	
	40						45					50				
ctg	tcc	act	aag	cct	caa	aac	tta	act	gcc	aca	acg	gac	gcc	gaa	gcc	307
Leu	Ser	Thr	Lys	Pro	Gln	Asn	Leu	Thr	Ala	Thr	Thr	Asp	Ala	Glu	Ala	
	55					60					65					
gct	tac	aaa	ggc	gca	gat	ttt	att	gtt	att	gca	acg	cca	act	aat	tac	355
Ala	Tyr	Lys	Gly	Ala	Asp	Phe	Ile	Val	Ile	Ala	Thr	Pro	Thr	Asn	Tyr	
	70				75					80					85	
gac	cca	gag	tca	aac	ttt	ttt	gat	act	tcc	agc	gtt	gag	tcc	gta	att	403
Asp	Pro	Glu	Ser	Asn	Phe	Phe	Asp	Thr	Ser	Ser	Val	Glu	Ser	Val	Ile	
				90					95					100		
gag	ata	gtc	ctt	aag	gtt	tct	cct	gga	tcc	aca	atc	gta	att	aaa	tcg	451
Glu	Ile	Val	Leu	Lys	Val	Ser	Pro	Gly	Ser	Thr	Ile	Val	Ile	Lys	Ser	
			105					110					115			
act	atc	cct	gtt	ggg	ttt	aca	tcg	gaa	cta	cgc	att	aag	cat	cca	gaa	499
Thr	Ile	Pro	Val	Gly	Phe	Thr	Ser	Glu	Leu	Arg	Ile	Lys	His	Pro	Glu	
		120					125					130				
gct	tcg	att	att	ttt	tca	cct	gag	ttc	ctg	cgt	gaa	ggc	cga	gca	ttc	547
Ala	Ser	Ile	Ile	Phe	Ser	Pro	Glu	Phe	Leu	Arg	Glu	Gly	Arg	Ala	Phe	
	135					140					145					
tac	gac	aat	ctc	tac	cca	tcc	aga	gtt	gtc	gtt	ggg	gat	cgc	agt	cct	595
Tyr	Asp	Asn	Leu	Tyr	Pro	Ser	Arg	Val	Val	Val	Gly	Asp	Arg	Ser	Pro	
	150				155					160					165	
ctg	ggg	gaa	gaa	ttt	gcg	act	ctg	tta	gct	gag	ggg	gca	aaa	gaa	aag	643
Leu	Gly	Glu	Glu	Phe	Ala	Thr	Leu	Leu	Ala	Glu	Gly	Ala	Lys	Glu	Lys	
				170					175					180		
cct	ccg	att	cta	ctt	acg	gac	tca	act	gag	gca	gag	gcg	att	aaa	tta	691
Pro	Pro	Ile	Leu	Leu	Thr	Asp	Ser	Thr	Glu	Ala	Glu	Ala	Ile	Lys	Leu	
			185					190					195			
ttt	tct	aat	aca	tat	ctt	gca	ctg	cga	gtt	gct	ttt	ttc	aac	gaa	ctg	739
Phe	Ser	Asn	Thr	Tyr	Leu	Ala	Leu	Arg	Val	Ala	Phe	Phe	Asn	Glu	Leu	
		200					205					210				
gat	act	tat	gcg	tct	gtt	cga	agc	ttg	gat	act	aag	cag	att	att	gaa	787
Asp	Thr	Tyr	Ala	Ser	Val	Arg	Ser	Leu	Asp	Thr	Lys	Gln	Ile	Ile	Glu	
	215					220					225					
ggg	gta	ggg	ctc	gat	cca	cgt	att	gga	tct	cat	tac	aat	aat	cct	tca	835
Gly	Val	Gly	Leu	Asp	Pro	Arg	Ile	Gly	Ser	His	Tyr	Asn	Asn	Pro	Ser	
	230				235					240					245	
ttt	gga	tat	ggc	gga	tat	tgt	ctt	ccg	aaa	gat	acg	aaa	cag	ctt	ctc	883
Phe	Gly	Tyr	Gly	Gly	Tyr	Cys	Leu	Pro	Lys	Asp	Thr	Lys	Gln	Leu	Leu	
				250				255						260		
gcc	aac	tat	aag	gat	gtc	ccg	cag	aat	cta	atc	tct	gca	gta	gtc	caa	931
Ala	Asn	Tyr	Lys	Asp	Val	Pro	Gln	Asn	Leu	Ile	Ser	Ala	Val	Val	Gln	
			265					270					275			

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa 979
 Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys
 280 285 290

 tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca 1027
 Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser
 295 300 305

 gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag 1075
 Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys
 310 315 320 325

 gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa 1123
 Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu
 330 335 340

 act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat 1171
 Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp
 345 350 355

 tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat 1219
 Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp
 360 365 370

 gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac 1261
 Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp
 375 380 385

 taagtggaaa gaatcttttg ttg 1284

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
 1 5 10 15

 Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
 20 25 30

 Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
 35 40 45

 Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
 50 55 60

 Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
 65 70 75 80

 Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
 85 90 95

 Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
 100 105 110

 Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
 115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
 275 280 285
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
 290 295 300
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
 305 310 315 320
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
 325 330 335
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
 340 345 350
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
 355 360 365
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
 370 375 380
 Gln Arg Asp
 385

<210> 273

<211> 1209

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA01377

<400> 273

tgaaatggat ttgctgcggc cccggaatta cccttttcgc ggccgtcatc aaatttgtag 60

ccccttaaag acaccctaaa cacgagtga ataggaacac atg act tta act gac 115
 Met Thr Leu Thr Asp
 1 5

aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc 163
 Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr
 10 15 20

cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act 211
 Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr
 25 30 35

gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca 259
 Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala
 40 45 50

ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc 307
 Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe
 55 60 65

gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat 355
 Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr
 70 75 80 85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc 403
 Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val
 90 95 100

tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg 451
 Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val
 105 110 115

ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac gcg gaa aag 499
 Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys
 120 125 130

gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg 547
 Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala
 135 140 145

ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt 595
 Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu
 150 155 160 165

gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac 643
 Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr
 170 175 180

gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt 691
 Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val
 185 190 195

tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga 739
 Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg
 200 205 210

gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca 787

Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
 215 220 225

agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
 230 235 240 245

tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883
 Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
 250 255 260

gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
 265 270 275

cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
 280 285 290

ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
 295 300 305

att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
 310 315 320 325

atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
 330 335 340

ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171
 Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg
 345 350 355

ttt tcg tct gat cag taggcatttt tagccctttt gga 1209
 Phe Ser Ser Asp Gln
 360

<210> 274

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val
 1 5 10 15

Gly Gly Lys Gly Thr Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys
 20 25 30

Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
 35 40 45

Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
 50 55 60

Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
 65 70 75 80

```
<210> 275
<211> 1350
<212> DNA
<213> Corynebacterium glutamicum
<220>
```

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

```

accgaaatgg gggcattaa aggggctatc attcggaccc caaaacgatg tttagacaat 60

ttgttaccca gctttcatgc gggatagtta ttttgccttt atg gtt aag ggt gtg 115
                                   Met Val Lys Gly Val
                                   1 5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                                   10 15 20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                                   25 30 35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                                   40 45 50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                                   55 60 65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                                   70 75 80 85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                                   90 95 100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                                   105 110 115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                                   120 125 130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                                   135 140 145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                                   150 155 160 165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                                   170 175 180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                                   185 190 195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

```

200	205	210	
cag gcg ctg aaa gat gat gaa aat aac gag aac agt gat cat gac atg			787
Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn Ser Asp His Asp Met			
215	220	225	
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt			835
Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val			
230	235	240	245
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag			883
Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys			
	250	255	260
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac			931
Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His			
	265	270	275
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag			979
Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu			
	280	285	290
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc			1027
Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe			
	295	300	305
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc			1075
Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile			
310	315	320	325
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc			1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val			
	330	335	340
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg			1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val			
	345	350	355
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac			1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn			
	360	365	370
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat			1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp			
	375	380	385
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag			1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys			
390	395	400	405
aac cag gta gtc taaacgggaa agggaccta aaa			1350
Asn Gln Val Val			

<210> 276

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
 1 5 10 15
 Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
 20 25 30
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
 35 40 45
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50 55 60
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65 70 75 80
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
 85 90 95
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
 100 105 110
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
 115 120 125
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
 130 135 140
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
 145 150 155 160
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
 165 170 175
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
 180 185 190
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
 195 200 205
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
 210 215 220
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
 225 230 235 240
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
 245 250 255
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
 260 265 270
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
 275 280 285
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
 290 295 300
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
 305 310 315 320
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

	325		330		335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val	340		345		350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala	355		360		365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val	370		375		380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val	385		390		395
Val Val Val Gly Lys Asn Gln Val Val	405				400

<210> 277

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN00014

<400> 277

catcaaagt accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaacttta ggcactaga ctaacaacac atg agc aaa tat gca	115
Met Ser Lys Tyr Ala	
1 5	

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc	163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile	
10 15 20	

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca	211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro	
25 30 35	

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc	259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu	
40 45 50	

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa	307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu	
55 60 65	

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac	355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp	
70 75 80 85	

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca	403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala	
90 95 100	

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc	451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile	

105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175	180	
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190	195	
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
tagactcccg gggttttgctt ggt			903

<210> 278

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Met	Ser	Lys	Tyr	Ala	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Glu	Leu	Ala	Glu
1				5				10						15	

Leu	Ala	Asp	Ser	Ile	Thr	Leu	Asp	Arg	Phe	Glu	Ala	Ser	Asp	Leu	Glu
		20						25					30		

Val	Ser	Ser	Lys	Pro	Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala
		35					40					45			

Thr	Glu	Glu	Ala	Leu	Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp
	50					55					60				

Ser	Ile	Leu	Gly	Glu	Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg
65					70					75					80

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro

			25				30				35							
gac	atg	act	ccc	gtc	agc	gat	gcc	gac	ctg	gcg	acc	gaa	gaa	gca	ctc	259		
Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala	Thr	Glu	Glu	Ala	Leu			
			40					45					50					
cgc	gag	aaa	atc	gcc	acc	gcc	cgc	ccc	gcc	gac	tcc	atc	ctc	ggt	gaa	307		
Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp	Ser	Ile	Leu	Gly	Glu			
			55					60					65					
gaa	ttc	ggt	ggc	gac	gta	gaa	ttc	agc	ggc	cgc	cag	tgg	atc	atc	gac	355		
Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg	Gln	Trp	Ile	Ile	Asp			
			70					75					80		85			
ccc	atc	gac	ggc	acc	aaa	aac	tac	gtc	cgc	ggc	gtc	ccc	gta	tgg	gca	403		
Pro	Ile	Asp	Gly	Thr	Lys	Asn	Tyr	Val	Arg	Gly	Val	Pro	Val	Trp	Ala			
			90								95		100					
acc	ctg	atc	gcg	ctg	ctc	gac	aac	ggc	aaa	ccc	gtc	gca	ggt	gtc	atc	451		
Thr	Leu	Ile	Ala	Leu	Leu	Asp	Asn	Gly	Lys	Pro	Val	Ala	Gly	Val	Ile			
			105					110					115					
tcc	gca	ccc	gca	ctg	gct	agg	cgt	tgg	tgg	gca	tcc	gaa	ggg	gcc	ggc	499		
Ser	Ala	Pro	Ala	Leu	Ala	Arg	Arg	Trp	Trp	Ala	Ser	Glu	Gly	Ala	Gly			
			120					125					130					
gca	tgg	cgc	acc	ttc	aac	ggc	agc	tcc	cca	cgc	aaa	ctg	tcc	gtg	tcc	547		
Ala	Trp	Arg	Thr	Phe	Asn	Gly	Ser	Ser	Pro	Arg	Lys	Leu	Ser	Val	Ser			
			135					140					145					
cag	gtg	tcc	aag	ctt	gac	gac	gcc	tcc	ctc	tcc	ttc	tcc	tcc	ctc	tcc	595		
Gln	Val	Ser	Lys	Leu	Asp	Asp	Ala	Ser	Leu	Ser	Phe	Ser	Ser	Leu	Ser			
			150		155			160						165				
ggc	tgg	gcc	gaa	cga	gat	ttg	cgc	gat	cag	ttc	gtc	tcc	cta	act	gat	643		
Gly	Trp	Ala	Glu	Arg	Asp	Leu	Arg	Asp	Gln	Phe	Val	Ser	Leu	Thr	Asp			
			170					175					180					
acc	acc	tgg	cga	ctc	cgc	ggc	tac	ggc	gac	ttc	ttc	tcc	tac	tgc	ctc	691		
Thr	Thr	Trp	Arg	Leu	Arg	Gly	Tyr	Gly	Asp	Phe	Phe	Ser	Tyr	Cys	Leu			
			185					190					195					
gtc	gcc	gaa	ggt	gcc	gtc	gat	atc	gcc	gct	gaa	cca	gaa	gtc	agc	ctc	739		
Val	Ala	Glu	Gly	Ala	Val	Asp	Ile	Ala	Ala	Glu	Pro	Glu	Val	Ser	Leu			
			200					205					210					
tgg	gat	ctt	gct	ccc	ctg	tcc	atc	ctg	gtc	acc	gaa	gcc	gga	gga	aag	787		
Trp	Asp	Leu	Ala	Pro	Leu	Ser	Ile	Leu	Val	Thr	Glu	Ala	Gly	Gly	Lys			
			215		220						225							
ttc	acc	tca	ctg	gct	ggc	gtc	gat	gga	cca	cac	ggt	ggc	gat	gca	gta	835		
Phe	Thr	Ser	Leu	Ala	Gly	Val	Asp	Gly	Pro	His	Gly	Gly	Asp	Ala	Val			
			230		235			240						245				
gcc	acc	aac	ggc	atc	ctg	cac	gat	gag	acg	ctg	gat	cgt	tta	aaa		880		
Ala	Thr	Asn	Gly	Ile	Leu	His	Asp	Glu	Thr	Leu	Asp	Arg	Leu	Lys				
			250						255					260				
tagactcccg ggttt																		

<210> 280
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280

```

Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
  1           5           10           15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
           20           25           30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
           35           40           45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
  50           55           60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
  65           70           75           80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
           85           90           95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
           100          105          110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
           115          120          125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
           130          135          140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
           145          150          155          160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
           165          170          175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
           180          185          190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
           195          200          205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
           210          215          220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
           225          230          235          240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
           245          250          255

Asp Arg Leu Lys
           260

```

<210> 281
 <211> 978
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01570

<400> 281

cactgaactc cgttttggat ctcggcaaaa tcgaagccac cggatttagc gcaccgacct 60

ggcagacccg cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
 Val Lys Gly Ile Ile
 1 5

ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
 Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
 10 15 20

tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
 Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
 25 30 35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
 Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
 40 45 50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
 Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
 55 60 65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
 Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
 70 75 80 85

cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
 Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
 90 95 100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
 Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
 105 110 115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
 His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
 120 125 130

tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
 Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
 135 140 145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
 Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
 150 155 160 165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
 Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
 170 175 180

atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
 Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
 185 190 195

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggtgtg gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
 280 285

<210> 282

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 282

Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
 1 5 10 15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
 20 25 30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
 130 135 140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
 145 150 155 160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
 165 170 175
 Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
 180 185 190
 Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
 195 200 205
 Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
 210 215 220
 Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
 225 230 235 240
 Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
 245 250 255
 Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
 260 265 270
 Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
 275 280 285

<210> 283

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> RXA02666

<400> 283

gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
 Met Ser Ser Thr Arg
 1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
 Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu
 10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
 25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
 40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
 55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg

70	75	80	85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt				403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891
<210> 284				
<211> 256				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 284				
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly				
1 5 10 15				
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu				
20 25 30				

```
<210> 285
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 285
cccgttcattg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60
tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
Met Arg Thr Val Val

	1										5					
acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc																163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile																
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc																211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg																
ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg																259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val																
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac																307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His																
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac																355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His																
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc																403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr																
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc																451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val																
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca																499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro																
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc																547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser																
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc																595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly																
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa																643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln																
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt																691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu																
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc																739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg																
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct																787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser																
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa																835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu																

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
 250 255 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
 265 270 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
 280 285 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 286
 <211> 311
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 286
 Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
 1 5 10 15
 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30
 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45
 Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60
 Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80
 Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95
 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110
 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125
 Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140
 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160
 Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 287
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> RXA01887

<400> 287
 catctttaca ggaaaccctt tgacggcatc aatgggtggt atctagtatc tactagaacg 60
 ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt 115
 Met Ser Val Lys Leu
 1 5
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile
 10 15 20
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr
 25 30 35
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser
 40 45 50
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile
 55 60 65

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
70 75 80 85	
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
 330 335

ttttaaaactc gca 1134

<210> 288

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn
 1 5 10 15

His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80

Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125

Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
 195 200 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220

Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240

Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala
 245 255

Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala
 260 265 270

Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu
 275 280 285

Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val
 290 295 300

Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile
 305 310 315 320

Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu
 325 330 335

Val

<210> 289
 <211> 996
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(973)
 <223> RXN00013

<400> 289
 ctgcagaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcctaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act 115
 Met Glu Gly Met Thr
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala

90										95					100					
gac	cgg	gcg	tcg	aaa	agc	gga	aaa	acc	tgg	gtc	atc	gac	ccg	gtt	gat	451				
Asp	Arg	Ala	Ser	Lys	Ser	Gly	Lys	Thr	Trp	Val	Ile	Asp	Pro	Val	Asp					
			105					110					115							
ggc	acc	tac	aac	ttc	acc	cag	ggc	tca	gat	tat	tgg	tgc	tcg	gcg	ctc	499				
Gly	Thr	Tyr	Asn	Phe	Thr	Gln	Gly	Ser	Asp	Tyr	Trp	Cys	Ser	Ala	Leu					
		120					125					130								
gcg	ctg	gtc	gag	ggc	gat	cca	tcc	gcg	cca	tcg	cgc	gtg	ctt	ttc	ggc	547				
Ala	Leu	Val	Glu	Gly	Asp	Pro	Ser	Ala	Pro	Ser	Arg	Val	Leu	Phe	Gly					
	135					140					145									
gcc	gta	cac	cgc	cca	gcc	atg	ggt	tat	acg	tgg	ttc	ggt	ggc	ccg	gga	595				
Ala	Val	His	Arg	Pro	Ala	Met	Gly	Tyr	Thr	Trp	Phe	Gly	Gly	Pro	Gly					
150					155				160					165						
atc	cgc	acc	acg	ctc	gac	ggc	aag	gag	cta	gat	ttg	ctt	gtc	gac	gcc	643				
Ile	Arg	Thr	Thr	Leu	Asp	Gly	Lys	Glu	Leu	Asp	Leu	Leu	Val	Asp	Ala					
				170					175					180						
ccc	ctc	aat	caa	atc	tcc	ctg	gcc	acc	tac	atc	cac	ccg	tca	cgc	atc	691				
Pro	Leu	Asn	Gln	Ile	Ser	Leu	Ala	Thr	Tyr	Ile	His	Pro	Ser	Arg	Ile					
			185					190					195							
gcg	gaa	cct	gat	att	caa	aag	gcg	tgg	atg	agc	gtt	gcc	acc	cac	cct	739				
Ala	Glu	Pro	Asp	Ile	Gln	Lys	Ala	Trp	Met	Ser	Val	Ala	Thr	His	Pro					
	200						205					210								
gca	acg	ctg	cgc	atg	ttc	ggc	gcc	ggc	tcc	atc	gat	ttg	gcc	aac	atc	787				
Ala	Thr	Leu	Arg	Met	Phe	Gly	Ala	Gly	Ser	Ile	Asp	Leu	Ala	Asn	Ile					
	215					220					225									
gcc	gac	ggc	agc	atg	ggc	gca	tgg	gtg	cag	cac	agc	gtc	gca	gat	tgg	835				
Ala	Asp	Gly	Ser	Met	Gly	Ala	Trp	Val	Gln	His	Ser	Val	Ala	Asp	Trp					
230					235				240					245						
gac	tgg	cta	ccc	ggc	cgc	gca	ctc	atc	gaa	ggc	gtc	ggc	gga	gca	tgc	883				
Asp	Trp	Leu	Pro	Gly	Arg	Ala	Leu	Ile	Glu	Gly	Val	Gly	Gly	Ala	Cys					
				250					255					260						
atc	aaa	gtg	acc	gcc	ggc	ggc	gtc	gaa	tgg	tcc	gtt	gca	gga	aac	gcg	931				
Ile	Lys	Val	Thr	Ala	Gly	Gly	Val	Glu	Trp	Ser	Val	Ala	Gly	Asn	Ala					
			265					270					275							
gaa	gca	gtt	agt	gag	atc	tcc	gaa	act	tta	agc	gca	cta	gac			973				
Glu	Ala	Val	Ser	Glu	Ile	Ser	Glu	Thr	Leu	Ser	Ala	Leu	Asp							
	280						285					290								
taacaacaca	tgagcaaata	tgc														996				

<210> 290

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu

1

5

10

15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
 165 170 175
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
 180 185 190
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
 195 200 205
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
 210 215 220
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
 225 230 235 240
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
 245 250 255
 Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
 260 265 270
 Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
 275 280 285
 Ala Leu Asp
 290

<210> 291

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00013

<400> 291

```

ctgcagaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act 115
                                         Met Glu Gly Met Thr
                                         1                               5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
                               10                               15                               20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
                               25                               30                               35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
                               40                               45                               50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
                               55                               60                               65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
                               70                               75                               80                               85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
                               90                               95                               100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
                               105                               110                               115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
                               120                               125                               130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
                               135                               140                               145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
                               150                               155                               160                               165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
                               170                               175                               180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
                               185                               190                               195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

```

Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
 280 285 290

tagcaacaca tgagcaaata tgc 996

<210> 292
 <211> 291
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 292
 Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160

[illegible]

```
<210> 293
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(925)  
<223> RXA01099
```

```

<400> 293
gggatgaggggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagaggct ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg 115
Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

```

```

gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc 355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
70 75 80 85

aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
90 95 100

gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
105 110 115

aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
120 125 130

cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
135 140 145

ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
150 155 160 165

cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
170 175 180

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
185 190 195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
200 205 210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
215 220 225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
230 235 240 245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
250 255 260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
265 270 275

taaaatgggc gtggcaattc gag 948

```

<210> 294

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
 1 5 10 15

Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
 20 25 30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
 35 40 45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
 50 55 60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65 70 75 80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
 85 90 95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
 100 105 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
 115 120 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
 260 265 270

Glu Tyr Lys
 275

<210> 295

<211> 576

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(576)

<223> RXN01332

<400> 295

cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct	48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala	
1 5 10 15	
gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct	96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala	
20 25 30	
atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag	144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln	
35 40 45	
ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc	192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile	
50 55 60	
ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc	240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile	
65 70 75 80	
gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc	288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe	
85 90 95	
atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa	336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu	
100 105 110	
tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac	384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn	
115 120 125	
cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc	432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser	
130 135 140	
gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt	480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val	
145 150 155 160	
gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc	528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser	
165 170 175	
ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg	576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val	
180 185 190	

<210> 296

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
 1 5 10 15
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
 20 25 30
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
 35 40 45
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
 50 55 60
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65 70 75 80
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
 85 90 95
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
 100 105 110
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
 115 120 125
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
 130 135 140
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
 145 150 155 160
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
 165 170 175
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
 180 185 190

<210> 297

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(549)

<223> FRXA01332

<400> 297

gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
 Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15

ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
 20 25 30

ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
	85	90	95
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
	100	105	110
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
	115	120	125
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
	130	135	140
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
	145	150	155
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
	165	170	175
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
	180		

<210> 298

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
1 5 10 15

Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
20 25 30

Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala
35 40 45

Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
50 55 60

Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys
65 70 75 80

Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn

	85		90		95	
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met 100 105 110						
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln 115 120 125						
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro 130 135 140						
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys 145 150 155 160						
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile 165 170 175						
Met Glu Leu Glu Asn Gly Val 180						
<210>	299					
<211>	1128					
<212>	DNA					
<213>	Corynebacterium glutamicum					
<220>						
<221>	CDS					
<222>	(101)..(1105)					
<223>	RXA01632					
<400>	299					
aagggctgcac acgtgctttc gacaccacca tcgcagcggt tgaacaagct gctcgtctcg	60					
ccccctccac taactgatct ttgaaaggct gaaaaaacat atg act ctt cgt atc	115					
				Met Thr Leu Arg Ile		
				1 5		
gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att	163					
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile						
		10 15 20				
gct gca aac cct gat ctt gaa ctg gtt gtt atc gcc gat cct ttc att	211					
Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile						
		25 30 35				
gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca	259					
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala						
		40 45 50				
tca cca gat gag gtg ttc gcc cgc gat gat atc gat gcc atc gtg atc	307					
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile						
		55 60 65				
ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa	355					
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu						
		70 75 80 85				
cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa	403					
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu						
		90 95 100				

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggg gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val	
330 335	

cct

1128

<210> 300

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

```

Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val
 1           5           10           15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile
      20           25           30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
      35           40           45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
      50           55           60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65           70           75           80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
      85           90           95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
      100          105          110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
      115          120          125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
      130          135          140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
 145          150          155          160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
      165          170          175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
      180          185          190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
      195          200          205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
 210          215          220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
 225          230          235          240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
      245          250          255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
      260          265          270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

```

275	280	285	
Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn			
290	295	300	
Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu			
305	310	315	320
Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val			
	325	330	335
<210> 301			
<211> 1206			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1183)			
<223> RXA01633			
<400> 301			
gcgaatgcat gccttgaatc agctcaaacc ggccgcaccg tcaccctcaa ccctgccaac 60			
gttttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115			
		Met Lys Asn Ile Thr	
		1 5	
atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac 163			
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn			
	10	15	20
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag 211			
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu			
	25	30	35
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg 259			
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala			
	40	45	50
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac 307			
Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp			
	55	60	65
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat 355			
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp			
	70	75	80
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag 403			
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys			
	90	95	100
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att 451			
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile			
	105	110	115
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac 499			
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp			
	120	125	130

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tggttt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtgtcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtgtac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
gggtac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctcgcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	
cgcctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat	883
Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp	
250 255 260	
gaagag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc	931
Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr	
265 270 275	
ggcgaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag	979
Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys	
280 285 290	
aatgag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac	1027
Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn	
295 300 305	
ccttgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca	1075
Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala	
310 315 320 325	
gctcag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta	1123
Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val	
330 335 340	
cgggaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg	1171
Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu	
345 350 355	
gttcca tct gct taaaacctta ctgcttatct aaa	1206
Val Pro Ser Ala	
360	

<210> 302

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
 1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
 115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
 180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
 225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr
 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
 260 265 270

Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe
 275 280 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu

[illegible]

Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala	
120 125 130	
ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga	547
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg	
135 140 145	
cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt	595
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly	
150 155 160 165	
ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc	643
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu	
170 175 180	
atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt	691
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu	
185 190 195	
cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa	739
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu	
200 205 210	
tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag	787
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu	
215 220 225	
tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac	835
Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn	
230 235 240 245	
tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc	883
Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr	
250 255 260	
aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc	931
Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr	
265 270 275	
ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat	979
Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp	
280 285 290	
tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc	1027
Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly	
295 300 305	
gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg	1075
Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu	
310 315 320 325	
gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc	1123
Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser	
330 335 340	
taaggagaag tgctgctggc tgc	1146
<210> 304	
<211> 341	
<212> PRT	

<213> Corynebacterium glutamicum

<400> 304

```

Met Thr Ile Arg Ile Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu
 1           5           10           15

Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly
          20           25           30

Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
          35           40           45

Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
 50           55           60

Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
 65           70           75           80

Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
          85           90           95

Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
          100          105          110

Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
 115          120          125

His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg
 130          135          140

Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala
 145          150          155          160

Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp
          165          170          175

Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu
          180          185          190

Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile
 195          200          205

Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys
 210          215          220

Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly
 225          230          235          240

Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln
          245          250          255

Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu
          260          265          270

Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro
 275          280          285

Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala
 290          295          300

Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala

```

305						310						315						320
Val	Leu	Lys	Val	Leu	Asp	Ala	Val	Ala	Gln	Ser	Ala	Ala	Glu	Lys	Arg			
				325					330					335				
Thr	Ile	Glu	Leu	Ser														
			340															
<210> 305																		
<211> 1200																		
<212> DNA																		
<213> Corynebacterium glutamicum																		
<220>																		
<221> CDS																		
<222> (101)..(1177)																		
<223> RXN01630																		
<400> 305																		
gtaggtgagt	cttcgtgaga	tacccccggc	cagtcataca	gttcaaccaa	gctccaccac	60												
ccagataaaa	acctgcgggg	tgcgttttag	gagaattccc	atg	agt	gat	caa	aaa								115		
				Met	Ser	Asp	Gln	Lys								5		
									1									
att	gtt	gtt	ggc	ctg	cta	ggc	atc	acc	cac	ccg	cat	gcg	tcg	gcg	cg	163		
Ile	Val	Val	Gly	Leu	Leu	Gly	Ile	Thr	His	Pro	His	Ala	Ser	Ala	Arg			
				10					15					20				
gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211		
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala			
				25				30					35					
gat	act	gat	tcc	cgc	ctc	cag	tac	ttc	acc	gac	aaa	tat	gat	gtt	gaa	259		
Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu			
			40				45					50						
ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307		
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile			
							60				65							
atg	gtt	cac	tcc	aag	agc	aag	gac	atg	gtc	cct	cac	gcc	aag	cgc	gcg	355		
Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala			
						75				80					85			
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403		
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr			
				90					95					100				
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451		
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro			
				105				110					115					
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499		
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val			
				120			125					130						
cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547		
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val			
							140				145							

```

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag 595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
150 155 160 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc 643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
170 175 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc 691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
185 190 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc 739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
200 205 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc 787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
215 220 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc 835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
230 235 240 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc 883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
250 255 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
265 270 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
280 285 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
295 300 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
310 315 320 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
330 335 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
345 350 355

aac atc taagaggagc actccatgaa acc 1200
Asn Ile

```

<210> 306

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

```

Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
 1          5          10          15

His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
          20          25          30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
          35          40          45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50          55          60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65          70          75          80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
          85          90          95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
          100          105          110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
          115          120          125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
          130          135          140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
          145          150          155          160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
          165          170          175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
          180          185          190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
          195          200          205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
          210          215          220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
          225          230          235          240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
          245          250          255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
          260          265          270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
          275          280          285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
          290          295          300

Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val

```

434

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa	547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
135 140 145	
gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc	595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
150 155 160 165	
atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc	643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
170 175 180	
cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc	691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
185 190 195	
cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat	739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
200 205 210	
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg	787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
215 220 225	
ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca	835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac	883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
250 255 260	
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac	931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt	979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
280 285 290	
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
295 300 305	
gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat	1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
310 315 320 325	
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag	1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
330 335 340	
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag	1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
345 350 355	
gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg	1212
Ala Phe Ile Ile Glu Ala	
360	

<210> 308
 <211> 363
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308

```

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
 1           5           10           15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
          20           25           30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
          35           40           45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
          50           55           60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
          65           70           75           80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
          85           90           95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
          100          105          110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
          115          120          125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
          130          135          140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
          145          150          155          160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
          165          170          175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
          180          185          190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
          195          200          205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
          210          215          220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
          225          230          235          240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
          245          250          255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
          260          265          270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
          275          280          285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

```

290	295	300	
Asp Ser Pro Asn Ser	Ala Gly Ile Ile Ile	Asp Ala Val Arg Ala Ala	
305	310	315	320
Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly	Pro Ile Met Pro Ala Ser		
	325	330	335
Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala			
	340	345	350
Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala			
	355	360	
<210> 309			
<211> 795			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(772)			
<223> RXN03057			
<400> 309			
catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60			
aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115			
		Leu Ala Ser Asp Leu	
		1 5	
ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163			
Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu			
	10	15	20
aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211			
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser			
	25	30	35
gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259			
Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile			
	40	45	50
gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307			
Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala			
	55	60	65
ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355			
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu			
	70	75	80
gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403			
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu			
	90	95	100
aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451			
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn			
	105	110	115
gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499			

Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220

aca 795

<210> 310

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
 1 5 10 15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155 160
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170 175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185 190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
	195	200 205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
	210	215 220

<210> 311
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> FRXA02902

<400> 311
 catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60
 aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115
 Leu Ala Ser Asp Leu
 1 5
 ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20
 aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35
 gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50
 gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65
 ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85
 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
 105 110 115
 gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499
 Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130
 gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145
 tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165
 ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180
 ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195
 tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210
 cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220
 aca 795

<210> 312

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
 1 5 10 15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

100	105	110
Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp		
115	120	125
Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp		
130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
165	170	175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
180	185	190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
195	200	205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
210	215	220

<210> 313

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXA00251

<400> 313

aaccagcggtt ttcagcgaga tactggacat atcaactaaa atccctgaat aaaacatcta 60

acatggggttt tatacagaaa attcatacga aaggttgatc atg aag aag aag att	115
Met Lys Lys Lys Ile	
1 5	

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa	163
Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys	
10 15 20	

gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag	211
Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu	
25 30 35	

cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc	259
His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser	
40 45 50	

gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa	307
Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys	
55 60 65	

aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt	355
---	-----

```

Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
70          75          80          85

gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
          90          95          100

gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc 451
Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
          105          110          115

gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499
Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
          120          125          130

ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac 547
Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
          135          140          145

gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
          150          155          160          165

ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
          170          175          180

ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691
Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
          185          190          195

tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739
Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
          200          205          210

gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
          215          220          225

gaa ctg gcg gac cgg aaa gat tagttctggg gggcttcctg ggc 831
Glu Leu Ala Asp Arg Lys Asp
          230          235

```

<210> 314

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

```

Met Lys Lys Lys Ile Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly
1          5          10          15

Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu
          20          25          30

Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
          35          40          45

Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
          50          55          60

```

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65 70 75 80
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
 85 90 95
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
 100 105 110
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
 115 120 125
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
 130 135 140
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
 145 150 155 160
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
 165 170 175
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
 180 185 190
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
 195 200 205
 Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
 210 215 220
 Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
 225 230 235

<210> 315

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXN02654

<400> 315

tattttcggg aatttataca gcaatcctcg aaatcctaataaagatccct tatcgtggga 60

gaggtacggg agttcgttcg aggacaacgt cgagaaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala		
		40					45					50					
ctt	att	act	ggg	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307	
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala		
	55					60					65						
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355	
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu		
	70				75					80					85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggg	caa	403	
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln		
				90					95					100			
aaa	gct	ttt	tct	ttc	cct	ggg	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451	
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg		
			105					110					115				
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggg	ggc	cta	gac	atc	ttg	499	
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu		
		120					125					130					
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggg	ttg	acc	gaa	att	547	
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile		
	135					140					145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggg	agt	595	
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser		
	150				155				160						165		
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643	
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser		
				170					175					180			
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691	
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
			185					190					195				
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739	
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly		
		200					205					210					
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787	
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
	215					220					225						
cca	ggg	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggg	cag	cca	caa	835	
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
	230				235					240					245		
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggg	883	
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly		
				250				255						260			
cac	cct	gtt	gag	ttg	gca	ggg	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931	
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu		
			265					270					275				
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggg	ggg	acg	ccc	979	
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro		

280 285 290

acc cca tagtcggtac aagcggaaatc act 1008

Thr Pro
295

<210> 316
<211> 295
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 316

Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp
1 5 10 15

Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
20 25 30

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
35 40 45

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
50 55 60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
65 70 75 80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
85 90 95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
100 105 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
115 120 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
130 135 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
145 150 155 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
165 170 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
180 185 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
195 200 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
210 215 220

Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
225 230 235 240

His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
245 250 255

gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg	259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val	
40 45 50	
gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct	307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser	
55 60 65	
gtt gtt ggg cgc ggt gga gga agc tgc gtt gct gga aat gcg atc ggt	355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly	
70 75 80 85	
gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat	403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp	
90 95 100	
att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt	451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys	
105 110 115	
gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg	499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro	
120 125 130	
gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
aat gcg tgt ggt tca cac tgc gtt gca ttc ggt aca gct gcg gaa aat	595
Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
150 155 160 165	
ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg	643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac	691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tgc ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
250 255 260	
ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg	931
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979

Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	Leu	Leu	
		280					285					290				
gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	aat	ctt	1027
Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	Asn	Leu	
		295				300					305					
cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	tgc	gag	1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
310					315					320					325	
aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
				330					335					340		
gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
			345					350					355			
gaa	atg	cgg	gaa	ttg	tgg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	att	gtc	1219
Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
		360					365					370				
acg	cgc	tta	gct	gat	ggc	ggg	gaa	gcg	tgg	ccg	aat	tgg	gaa	gac	tcg	1267
Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
		375				380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggc	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
			425					430					435			
ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
		440					445					450				
gcg	tct	tat	ggc	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggc	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
		455				460					465					
cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tgg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
			505					510					515			
ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	

520	525	530	
gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt gta tcc Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly Val Ser 535 540 545			1747
gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa atc acc Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln Ile Thr 550 555 560 565			1795
ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc tct gag Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu Ser Glu 570 575 580			1843
atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa gaa gtc Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu Glu Val 585 590 595			1891
aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca tcg gaa Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala Ser Glu 600 605 610			1939
tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc ctg gac Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe Leu Asp 615 620 625			1987
aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc atg ggc Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val Met Gly 630 635 640 645			2035
tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro 650 655 660			2083
acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca gtg gtg Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro Val Val 665 670 675			2131
cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His 680 685 690			2179
cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val 695 700 705			2227
gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala 710 715 720 725			2275
cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile 730 735 740			2323
cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln 745 750 755			2371
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys 760 765 770			2419

ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc 2467
 Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
 775 780 785

 acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat 2515
 Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
 790 795 800 805

 ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca 2563
 Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
 810 815 820

 cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa 2611
 Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
 825 830 835

 tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac 2659
 Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
 840 845 850

 cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa 2707
 Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
 855 860 865

 caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
 870 875 880 885

 aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
 890 895 900

 ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc 2851
 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
 905 910 915

 tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt 2899
 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
 920 925 930

 gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
 Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln
 935 940 945

 taacgatcat gcaacaggtg ctc 2967

<210> 132

<211> 948

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Thr His Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser
 1 5 10 15

Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
 20 25 30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala

35					40					45					
Glu	Pro	Glu	Asn	Val	Glu	Gln	Ile	Arg	Asp	Ala	Ile	Ala	Val	Ala	Val
50					55					60					
Ala	Arg	Gly	Trp	Ser	Val	Val	Gly	Arg	Gly	Gly	Gly	Ser	Ser	Val	Ala
65					70					75					80
Gly	Asn	Ala	Ile	Gly	Glu	Gly	Leu	Ile	Ile	Asp	Thr	Ser	Arg	Tyr	Phe
				85					90					95	
Asn	Arg	Ile	Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu
			100					105					110		
Pro	Gly	Val	Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly
		115					120					125			
Leu	Thr	Tyr	Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly
		130				135					140				
Gly	Met	Val	Ala	Asn	Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly
145					150					155					160
Thr	Ala	Ala	Glu	Asn	Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly
				165					170					175	
Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn
			180					185					190		
Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys
		195					200					205			
Glu	Leu	Gly	Arg	Phe	Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr
		210				215					220				
Leu	Ala	His	Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile
225					230					235					240
Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val
				245					250					255	
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg
			260					265					270		
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met
		275					280					285			
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu
		290				295					300				
Ala	Gly	Gln	Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly
305					310					315					320
Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln
				325					330					335	
Ala	Ala	Glu	Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val
			340					345					350		
Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser
		355					360					365			

Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro
 370 375 380
 Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
 385 390 395 400
 Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
 405 410 415
 Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
 420 425 430
 Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
 435 440 445
 Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
 450 455 460
 Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
 465 470 475 480
 Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
 485 490 495
 Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
 500 505 510
 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525
 His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540
 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
 545 550 555 560
 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
 565 570 575
 Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590
 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605
 Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
 610 615 620
 Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
 625 630 635 640
 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655
 Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
 660 665 670
 Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
 675 680 685


```

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
 690                               695                               700

Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
 705                               710                               715                               720

Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
                               725                               730                               735

Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
                               740                               745                               750

His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
                               755                               760                               765

Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
 770                               775                               780

Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
 785                               790                               795                               800

Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
                               805                               810                               815

Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
                               820                               825                               830

Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
 835                               840                               845

Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
 850                               855                               860

Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
 865                               870                               875                               880

Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
                               885                               890                               895

Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
 900                               905                               910

Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
 915                               920                               925

Gln Ala Thr His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn
 930                               935                               940

Asn Met Ala Gln
945

```

```

<210> 133
<211> 2858
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (1)..(2835)
<223> FRXA00296

```

<400> 133

acc atc aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct	48
Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser	
1 5 10 15	
cgc gcg aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct	96
Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser	
20 25 30	
gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa	144
Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu	
35 40 45	
aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg	192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly	
50 55 60	
tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg	240
Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala	
65 70 75 80	
atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att	288
Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile	
85 90 95	
tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg	336
Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val	
100 105 110	
gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac	384
Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr	
115 120 125	
ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt	432
Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val	
130 135 140	
gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg	480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala	
145 150 155 160	
gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc	528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val	
165 170 175	
act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc	576
Thr Val Thr Lys Asp Gly Cys Asp Ala Glu Ile Asn Gln Lys Leu	
180 185 190	
acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt	624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly	
195 200 205	
cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac	672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His	
210 215 220	
gac atg gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att	720
Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile	
225 230 235 240	

act	cgg	ttg	acg	gtg	aag	ttg	gtt	cca	aca	ccc	aaa	gtg	aaa	gcg	ctt	768
Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu	
				245					250					255		
gct	gtc	ctg	gct	ttc	gac	acg	gtt	ttt	gac	gcc	gcc	cga	gca	gcc	gcc	816
Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg	Ala	Ala	Ala	
			260					265					270			
aaa	ttg	cga	ctg	cct	ggg	gta	gca	acc	att	gaa	ggc	atg	ggc	gga	gat	864
Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	
			275				280					285				
ctc	ctc	gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	912
Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	
			290				295					300				
aat	ctt	cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	960
Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	
					310					315					320	
tgc	gag	aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	1008
Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	
				325					330					335		
gaa	gtc	gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	1056
Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	
			340					345					350			
cct	tct	gaa	atg	cgg	gaa	ttg	tgg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	1104
Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	
			355				360					365				
att	gtc	acg	cgc	tta	gct	gat	ggg	ggg	gaa	gcg	tgg	ccg	aat	tgg	gaa	1152
Ile	Val	Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	
			370				375				380					
gac	tcg	gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	1200
Asp	Ser	Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	
					390					395					400	
tat	gcg	ctg	atg	gat	aag	ttc	gat	tac	cag	ggg	att	cca	ttt	gga	cac	1248
Tyr	Ala	Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	
				405					410					415		
ttt	gga	gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	1296
Phe	Gly	Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	
			420					425					430			
aag	gaa	ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	1344
Lys	Glu	Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	
			435				440					445				
ttg	gtg	gcg	tct	tat	ggg	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggg	1392
Leu	Val	Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	
			450				455				460					
cgc	gcc	cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	1440
Arg	Ala	Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	
					470					475					480	

gca ctc ttc gaa gaa ttc aag ctg att ttc gat ccc cag cgc atc ttc	1488
Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
485 490 495	
aat ccg gga gtg ttg gtc tgg gca gat cct gtc atg caa gga ctt cgc	1536
Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
500 505 510	
atg gac ccg ggc cag cgc gcc ctc gac atc acg ccc gta cac aaa ttc	1584
Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
515 520 525	
tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt	1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
530 535 540	
gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa	1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
545 550 555 560	
atc acc ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc	1728
Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
565 570 575	
tct gag atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa	1776
Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
580 585 590	
gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca	1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
595 600 605	
tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc	1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
610 615 620	
ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
625 630 635 640	
atg ggc tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt	1968
Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
645 650 655	
ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca	2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
660 665 670	
gtg gtg cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc	2064
Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
675 680 685	
gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
690 695 700	
acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga	2160
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
705 710 715 720	
cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208

Pro	Ala	His	Ala	Ala	Ile	Lys	Thr	Leu	Glu	Ala	Leu	Gly	Tyr	Asn	Val		
				725					730					735			
gtc	atc	cca	gat	ggc	ttc	gtc	tgc	tgt	gga	ctc	acc	tgg	cat	tcc	acc	2256	
Val	Ile	Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr		
			740					745					750				
ggc	caa	ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	2304	
Gly	Gln	Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val		
			755				760					765					
atg	aaa	ccc	tac	ctg	gac	caa	ggg	cta	aca	gtc	gtt	ggg	ttg	gaa	cct	2352	
Met	Lys	Pro	Tyr	Leu	Asp	Gln	Gly	Leu	Thr	Val	Val	Gly	Leu	Glu	Pro		
	770					775					780						
tcg	tgc	acc	gtc	atg	ctt	caa	gat	gag	gca	aca	gaa	ctc	tcc	gat	aac	2400	
Ser	Cys	Thr	Val	Met	Leu	Gln	Asp	Glu	Ala	Thr	Glu	Leu	Ser	Asp	Asn		
785					790				795						800		
cct	gat	ctg	gca	cgc	ctt	gca	gca	ctg	acc	aaa	cca	ttc	gct	gag	gtc	2448	
Pro	Asp	Leu	Ala	Arg	Leu	Ala	Ala	Leu	Thr	Lys	Pro	Phe	Ala	Glu	Val		
				805					810					815			
atc	gca	cca	aag	atc	acc	gag	cta	gtc	gag	tct	gga	agc	ctc	cag	cta	2496	
Ile	Ala	Pro	Lys	Ile	Thr	Glu	Leu	Val	Glu	Ser	Gly	Ser	Leu	Gln	Leu		
			820					825					830				
aca	gaa	tca	act	gcg	ctt	acc	cag	gtg	cac	tgc	cac	gag	cgt	tcg	cta	2544	
Thr	Glu	Ser	Thr	Ala	Leu	Thr	Gln	Val	His	Cys	His	Glu	Arg	Ser	Leu		
			835				840					845					
ggc	gac	cca	caa	caa	tcg	gca	ctc	gtt	ctt	gaa	gct	ttg	ggg	gta	aaa	2592	
Gly	Asp	Pro	Gln	Gln	Ser	Ala	Leu	Val	Leu	Glu	Ala	Leu	Gly	Val	Lys		
	850					855					860						
gat	gaa	caa	att	gcc	act	ggg	tgt	tgc	ggg	ctt	gcc	gga	aac	tgg	ggc	2640	
Asp	Glu	Gln	Ile	Ala	Thr	Gly	Cys	Cys	Gly	Leu	Ala	Gly	Asn	Trp	Gly		
865				870					875						880		
ttt	gaa	aaa	gac	cac	gct	gaa	atg	tcc	ttc	gca	ctt	ggg	gaa	cga	gag	2688	
Phe	Glu	Lys	Asp	His	Ala	Glu	Met	Ser	Phe	Ala	Leu	Gly	Glu	Arg	Glu		
				885					890					895			
ctg	ttc	ccc	aag	gtc	aga	aaa	gca	gaa	gga	cat	gtg	att	gct	gac	ggg	2736	
Leu	Phe	Pro	Lys	Val	Arg	Lys	Ala	Glu	Gly	His	Val	Ile	Ala	Asp	Gly		
			900					905					910				
ttc	tcc	tgc	cgc	acc	cag	atc	gaa	caa	ggc	acc	gga	aaa	caa	gca	acg	2784	
Phe	Ser	Cys	Arg	Thr	Gln	Ile	Glu	Gln	Gly	Thr	Gly	Lys	Gln	Ala	Thr		
			915				920					925					
cac	ctt	gca	gag	gtg	gtc	tta	agc	atc	ttg	gag	caa	aac	aac	atg	gca	2832	
His	Leu	Ala	Glu	Val	Val	Leu	Ser	Ile	Leu	Glu	Gln	Asn	Asn	Met	Ala		
	930					935					940						
caa	taacgatcat	gcaacaggtg	ctc													2858	
Gln																	
945																	

<210> 134

<211> 945

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

```

Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser
 1           5           10           15

Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser
          20           25           30

Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
          35           40           45

Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
          50           55           60

Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
          65           70           75           80

Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
          85           90           95

Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
          100          105          110

Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
          115          120          125

Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
          130          135          140

Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
          145          150          155          160

Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
          165          170          175

Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
          180          185          190

Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
          195          200          205

Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
          210          215          220

Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
          225          230          235          240

Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
          245          250          255

Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
          260          265          270

Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
          275          280          285

Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
          290          295          300

```

Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
 305 310 315 320
 Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
 325 330 335
 Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
 340 345 350
 Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
 355 360 365
 Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
 370 375 380
 Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
 385 390 395 400
 Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
 405 410 415
 Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
 420 425 430
 Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
 435 440 445
 Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
 450 455 460
 Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
 465 470 475 480
 Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
 485 490 495
 Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
 500 505 510
 Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
 515 520 525
 Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
 530 535 540
 Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
 545 550 555 560
 Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
 565 570 575
 Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
 580 585 590
 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
 595 600 605
 Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
 610 615 620

Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
 625 630 635 640
 Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
 645 650 655
 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
 660 665 670
 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
 675 680 685
 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
 690 695 700
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
 705 710 715 720
 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
 725 730 735
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
 740 745 750
 Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
 755 760 765
 Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
 770 775 780
 Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
 785 790 795 800
 Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
 805 810 815
 Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
 820 825 830
 Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
 835 840 845
 Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
 850 855 860
 Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
 865 870 875 880
 Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
 885 890 895
 Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
 900 905 910
 Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
 915 920 925
 His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
 930 935 940
 Gln

945

<210> 135

<211> 1383

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1360)

<223> RXA01901

<400> 135

```

gcatgttgcc ttctctctgt gatcgccctcg ttcttcatcc aacgcgtcgc gcaccaagag 60

aactaaaatc taagtaaaac ccctccgaaa ggaaccaccc atg gtg aaa cgt caa 115
                               Met Val Lys Arg Gln
                               1           5

ctg ccc aac ccc gca gaa cta ctc gaa ctc atg aag ttc aaa aag cca 163
Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro
                               10           15           20

gag ctc aac ggc aag aaa cga cgc cta gac tcc gcg ctc acc atc tac 211
Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr
                               25           30           35

gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac 259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Ala Phe Asp
                               40           45           50

tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt 307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg
                               55           60           65

gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca 355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala
                               70           75           80           85

gaa cac gta gac acc acc acc caa atc ctg ggc gga acc tcc tcc atg 403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met
                               90           95           100

cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa 451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu
                               105           110           115

ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc 499
Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala Ala Gly Ile Pro Phe
                               120           125           130

acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc 547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr
                               135           140           145

aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc 595
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg
                               150           155           160           165

gaa atc tcc tac ggc ctc gtc gaa cgc gca gcc aaa gca gga ttc gac 643

```

Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala Lys Ala Gly Phe Asp	
170 175 180	
acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc	691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg	
185 190 195	
gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc	739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr	
200 205 210	
gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc	787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr	
215 220 225	
acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg	835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser Thr Gly Gly Thr Val	
230 235 240 245	
ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac	883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp	
250 255 260	
ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt	931
Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly	
265 270 275	
gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac	979
Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp	
280 285 290	
ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca	1027
Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro	
295 300 305	
gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa	1075
Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu	
310 315 320 325	
cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc	1123
Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val	
330 335 340	
gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac	1171
Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr	
345 350 355	
ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc	1219
Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile	
360 365 370	
gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt	1267
Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val	
375 380 385	
tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag	1315
Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys	
390 395 400 405	
atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att	1360
Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile	

410 415 420
 taaaagtttc tctccttagc tat 1383

<210> 136
 <211> 420
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 136
 Met Val Lys Arg Gln Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met
 1 5 10 15
 Lys Phe Lys Lys Pro Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser
 20 25 30
 Ala Leu Thr Ile Tyr Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro
 35 40 45
 Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser
 50 55 60
 Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp
 65 70 75 80
 Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly
 85 90 95
 Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg
 100 105 110
 Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala
 115 120 125
 Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu
 130 135 140
 Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr
 145 150 155 160
 Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala
 165 170 175
 Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala
 180 185 190
 Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln
 195 200 205
 Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp
 210 215 220
 Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser
 225 230 235 240
 Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr
 245 250 255
 Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys
 260 265 270

Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu
 275 280 285
 Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln
 290 295 300
 Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys
 305 310 315 320
 Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn
 325 330 335
 Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu
 340 345 350
 Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly
 355 360 365
 Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met
 370 375 380
 Ala Leu Leu Gly Val Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val
 385 390 395 400
 Thr Gln Leu Ala Lys Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala
 405 410 415
 Ala Ala Glu Ile
 420

<210> 137
 <211> 1836
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1813)
 <223> RXN01952

<400> 137
 ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60
 tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
 Met Thr Gln Pro Gly
 1 5
 cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
 10 15 20
 gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
 25 30 35
 agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac	307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp	
55 60 65	
aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt	355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly	
70 75 80 85	
gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc	403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile	
90 95 100	
tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag	451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu	
105 110 115	
gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc	499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu	
120 125 130	
gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc	547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile	
135 140 145	
ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag	595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
150 155 160 165	
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc	643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
170 175 180	
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
185 190 195	
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027

Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu	Pro	Ile	Ser	Gly	Glu		
295						300					305						
tac	atg	ggc	cgc	agt	gcc	ttc	gac	ttg	gcc	gag	aag	tac	ggc	aaa	gac	1075	
Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp		
310					315					320					325		
acc	ttc	gtc	ttc	ctg	aag	ttc	atg	agt	cca	gcg	ctg	cag	acg	cgc	atg	1123	
Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met		
				330					335					340			
ttc	tcg	ttc	aag	acg	tgg	gcc	aac	ggc	ttg	ttc	tcg	aag	att	ccc	ggc	1171	
Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly		
			345					350					355				
att	ggt	ccg	acc	ttc	gcc	gac	acg	gta	tcg	caa	gcc	atg	ttc	agc	gtg	1219	
Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val		
		360					365					370					
ctg	ccc	aac	cag	ctg	ccc	aag	cgc	atg	atg	gag	tac	cgc	aac	cgt	ttc	1267	
Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe		
	375					380					385						
gag	cat	cac	ctg	ctg	ctc	acc	gtc	agc	gag	tcg	cag	aag	gcc	gcg	agc	1315	
Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser		
390					395				400						405		
gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggt	gag	1363	
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu		
			410					415						420			
ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411	
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg		
			425				430						435				
ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459	
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg		
		440					445					450					
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507	
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp		
	455					460					465						
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555	
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu		
470					475				480						485		
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603	
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp		
			490						495					500			
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651	
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile		
		505					510						515				
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699	
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn		
		520					525					530					
tac	ggt	cgc	atg	tac	aag	ctg	ccg	gag	tcc	atg	gaa	gag	cac	ttc	aag	1747	
Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met	Glu	Glu	His	Phe	Lys		

535					540					545							
gag	ctc	gat	ccg	acg	aat	acg	ttc	aac	gcc	ggt	atc	ggc	ggc	acg	tcg	1795	
Glu	Leu	Asp	Pro	Thr	Asn	Thr	Phe	Asn	Ala	Gly	Ile	Gly	Gly	Thr	Ser		
550					555					560					565		
ccg	cac	aag	gac	tgg	gcc	taagtcccca					aggtagcgcg					acg	1836
Pro	His	Lys	Asp	Trp	Ala												
570																	

```
<210> 138
<211> 571
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 138															
Met	Thr	Gln	Pro	Gly	Gln	Thr	Thr	Thr	Thr	Ser	His	Glu	Ala	Ile	Asp
1				5					10					15	
Ala	Phe	Lys	Arg	Ile	Val	Gly	Asp	Glu	His	Val	Leu	Thr	Ser	Glu	Arg
			20					25					30		
Ala	Thr	Met	Pro	Phe	Ser	Lys	Gly	Tyr	Arg	Phe	Gly	Gly	Gly	Pro	Val
		35					40					45			
Phe	Ala	Val	Val	Arg	Pro	Gly	Thr	Leu	Val	Glu	Met	Trp	Arg	Ala	Leu
	50					55					60				
Gln	Val	Ser	Val	Asp	Asn	Asn	Leu	Ile	Val	Ile	Pro	Gln	Ala	Ser	Asn
65					70					75					80
Thr	Gly	Leu	Thr	Gly	Gly	Ser	Gly	Pro	Gly	Phe	Gln	Asp	Tyr	Asp	Arg
				85					90					95	
Pro	Ile	Val	Ile	Ile	Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile
			100					105					110		
Asn	Asp	Ala	Arg	Glu	Ala	Ile	Ser	Leu	Ala	Gly	Thr	Pro	Leu	Thr	His
		115					120					125			
Leu	Thr	Asp	Ala	Leu	Ala	Lys	His	Gln	Arg	Glu	Pro	His	Ser	Val	Ile
	130					135					140				
Gly	Ser	Thr	Ser	Ile	Gly	Ala	Ser	Val	Ile	Gly	Gly	Ile	Ala	Asn	Asn
145					150					155					160
Ser	Gly	Gly	Ser	Gln	Ile	Arg	Lys	Gly	Pro	Ala	Phe	Thr	Arg	Glu	Ala
				165					170					175	
Ile	Phe	Ala	Arg	Val	Asn	Asp	Asp	Gly	Lys	Val	Glu	Leu	Val	Asn	His
			180					185					190		
Leu	Gly	Ile	Ser	Leu	Gly	Asp	Asp	Pro	Glu	Val	Ala	Leu	Asp	Arg	Leu
		195					200					205			
Gln	Arg	Gly	Glu	Trp	Ser	Pro	Glu	Asp	Val	Thr	Pro	Ala	Pro	Glu	Asp
	210					215					220				
Ser	Asn	Glu	Thr	Glu	Tyr	Ala	Glu	His	Leu	Arg	Lys	Ile	Val	Pro	Ser
225					230					235					240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
 485 490 495
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
 500 505 510
 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
 515 520 525
 Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
 530 535 540
 Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly
 545 550 555 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala
565 570

<210> 139
<211> 239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(216)
<223> FRXA01952

<400> 139
cca gga cta tgt cgc caa gca ggg cgt gga tct caa ggc gct gac gac 48
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
1 5 10 15
cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag 96
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
20 25 30
cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac 144
His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
35 40 45
ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc 192
Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
50 55 60
acg tcg ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 239
Thr Ser Pro His Lys Asp Trp Ala
65 70

<210> 140
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
1 5 10 15
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
20 25 30
His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
35 40 45
Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
50 55 60
Thr Ser Pro His Lys Asp Trp Ala
65 70

<210> 141
<211> 1699
<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1699)

<223> FRXA01955

<400> 141

```

ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60
tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
                                         Met Thr Gln Pro Gly
                                         1 5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr 10 Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile 20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe 25 30 35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp 55 60 65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly 70 75 80 85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile 90 95 100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu 105 110 115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu 120 125 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile 135 140 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag 595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln 150 155 160 165

att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc 643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val 170 175 180

aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc 691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu 185 190 195

```

gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser	
390 395 400 405	
gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag	1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu	
410 415 420	
ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg	1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg	
425 430 435	

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450
 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465
 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485
 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500
 tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515
 cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac 1699
 Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
 520 525 530

<210> 142

<211> 533

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
 1 5 10 15
 Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30
 Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
 35 40 45
 Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60
 Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80
 Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95
 Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110
 Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125
 Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140
 Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175
 Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190
 Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205
 Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220
 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240
 Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His

222

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc 547
 Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
 135 140 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt 595
 Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
 150 155 160 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc 643
 Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
 170 175 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg 691
 Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
 185 190 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc 739
 Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
 200 205 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc 787
 Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
 215 220 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
 230 235 240 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
 250 255 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
 265 270 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
 280 285 290

atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 295 300

tag 1035

<210> 144

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Lys Ile Phe Val Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala
 1 5 10 15

Leu Lys Glu Ala Gly Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu
 20 25 30

Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro
 35 40 45

Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
 50 55 60
 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
 65 70 75 80
 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
 85 90 95
 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
 100 105 110
 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
 115 120 125
 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
 130 135 140
 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
 145 150 155 160
 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
 165 170 175
 Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
 180 185 190
 Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
 195 200 205
 Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
 210 215 220
 Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
 245 250 255
 Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
 260 265 270
 Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
 275 280 285
 Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 290 295 300

<210> 145

<211> 687

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (62)..(664)

<223> RXN01130

<400> 145

agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
 Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
 20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
 Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
 35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
 Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
 Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
 Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
 85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
 Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
 100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
 Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
 115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
 Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
 130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
 Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
 145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
 Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
 165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
 Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
 180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
 Ala Thr Ser Phe Gln Val Asp Leu Asp
 195 200

tga 687

<210> 146

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 146

```

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1           5           10           15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20           25           30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35           40           45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
  50           55           60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
  65           70           75           80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85           90           95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100          105          110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115          120          125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130          135          140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145          150          155          160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165          170          175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180          185          190

Ala Thr Ser Phe Gln Val Asp Leu Asp
      195          200

```

<210> 147

<211> 326

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(303)

<223> FRXA01130

<400> 147

```

gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc   48
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
  1           5           10           15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg   96

```

Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30
 cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg 144
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45
 ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag 192
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60
 aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct 240
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80
 gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc 288
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95
 cag gtt gat ctt gac taattagaga tccatttgct tga 326
 Gln Val Asp Leu Asp
 100

<210> 148
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 148
 Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1 5 10 15
 Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95
 Gln Val Asp Leu Asp
 100

<210> 149
 <211> 604
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(604)
 <223> RXN03112

<400> 149

```

gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcgggtcttc tttcaacggg  gtg gaa att ttc gga 115
                               Val Glu Ile Phe Gly
                               1           5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
                10                15                20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
                25                30                35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
                40                45                50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
                55                60                65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
                70                75                80                85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
                90                95                100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
                105                110                115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
                120                125                130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
                135                140                145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
                150                155                160                165

gcg ctg gct
Ala Leu Ala
604

```

<210> 150

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 150

```

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1           5           10          15

```

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
 20 25 30
 Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
 35 40 45
 Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
 50 55 60
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
 65 70 75 80
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
 85 90 95
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160
 Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 151
 <211> 649
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(649)
 <223> FRXA01133

<400> 151
 tgtttctagt cgacgccaa aaccggcgt ggacacgtct gcagccgacg cggtcgtgcc 60
 tgttgtagac ggacattcct agtttttcca ggagtaactt gtg agc cag aat ggc 115
 Val Ser Gln Asn Gly
 1 5
 cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163
 Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp
 10 15 20
 gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211
 Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg
 25 30 35
 cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt 259
 Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg
 40 45 50

```

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
    55                60                65

aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
    70                75                80                85

gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
                90                95                100

att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
                105                110                115

cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
                120                125                130

ggg ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg 547
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
    135                140                145

tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
    150                155                160                165

ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
                170                175                180

gcg ggt
Ala Gly
649

```

<210> 152

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 152

```

Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
    1                5                10                15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
    20                25                30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
    35                40                45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
    50                55                60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
    65                70                75                80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
    85                90                95

```

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
 165 170 175

Leu Thr Leu Leu Arg Ala Gly
 180

<210> 153

<211> 1011

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(988)

<223> RXN00871

<400> 153

gggaaaaggc gatcaccagc cggtggctcg acccagcaac ccacgggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451

Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
 105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
 Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
 120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
 Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
 135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
 Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
 150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
 Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
 170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
 Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
 185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
 Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
 200 205 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787
 Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
 215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835
 Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
 230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883
 Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
 250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931
 Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
 265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979
 Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn
 280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011
 Lys Glu Gly
 295

<210> 154

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
 1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

```

gggaaaaggc gatcaccagc cggtggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
                                         Met Arg Trp Phe His
                                         1           5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
                        10                        15                        20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
                        25                        30                        35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
                        40                        45                        50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
                        55                        60                        65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
                        70                        75                        80                        85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
                        90                        95                        100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
                        105                        110                        115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
                        120                        125                        130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
                        135                        140                        145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
                        150                        155                        160                        165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
                        170                        175                        180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
                        185                        190                        195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

```

200	205	210	
cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc			787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile			
215	220	225	
gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc			835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly			
230	235	240	245
tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga			883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg			
250	255	260	
atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca			931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr			
265	270	275	
tgg acc ggg caa gca ttt gat gat cgc ttg cca			964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro			
280	285		

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln			
1	5	10	15
Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg			
20	25	30	
Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly			
35	40	45	
Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His			
50	55	60	
His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly			
65	70	75	80
Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser			
85	90	95	
Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys			
100	105	110	
Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly			
115	120	125	
Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala			
130	135	140	
Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu			
145	150	155	160
Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly			
165	170	175	

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285

<210> 157
 <211> 373
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXN02829

<400> 157
 tttttcgttt aatctcatat ttaaacacgt tccttttaat tgggtttata aattgataaa 60
 ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5
 cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20
 tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35
 gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50
 gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65
 gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

```
<400> 159
tttttcggtt aaatctatat ttaaacacgt tccttttaat tgggtttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaaag gagactggac atg caa aaa aat att    115
                                         Met Gln Lys Asn Ile
                                           1                      5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt    163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
                        10                          15                  20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att    211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
                        25                          30                  35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga    259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
                40                          45                  50
```

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
 70 75 80 85

gga cat atg acg tgg gga tcc 376
 Gly His Met Thr Trp Gly Ser
 90

<210> 160

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
 1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
 20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
 35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
 50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65 70 75 80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
 85 90

<210> 161

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXN01468

<400> 161

tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115
 Met Thr Val Asn Ile
 1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
 Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
 10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
 Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

25						30						35					
gag	ttt	atg	gtt	ttg	acc	aac	aac	tcc	att	ttc	acc	ccg	agg	gat	ctt	259	
Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe	Thr	Pro	Arg	Asp	Leu		
		40					45					50					
tct	gca	cgt	ctt	aag	act	tcc	ggg	ttg	gat	atc	ccg	ccg	gag	cgt	att	307	
Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile	Pro	Pro	Glu	Arg	Ile		
		55					60					65					
tgg	act	tct	gca	acc	gcc	act	gct	cac	ttc	ctg	aaa	tcc	cag	gtc	aag	355	
Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu	Lys	Ser	Gln	Val	Lys		
		70					75					80				85	
gag	ggc	aca	gcc	tat	gtt	gtt	ggc	gag	tcc	ggg	ctg	acc	act	gcg	ttg	403	
Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly	Leu	Thr	Thr	Ala	Leu		
				90					95					100			
cat	acc	gcg	ggg	tgg	att	ttg	acg	gat	gca	aat	cct	gag	ttt	gtt	gtc	451	
His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn	Pro	Glu	Phe	Val	Val		
				105					110					115			
ctg	ggc	gaa	acc	cgc	aca	tat	tcc	ttc	gag	gca	atc	act	act	gcg	ata	499	
Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala	Ile	Thr	Thr	Ala	Ile		
				120					125					130			
aat	ctg	att	ttg	ggg	ggc	gct	cgc	ttt	att	tgc	acc	aac	ccg	gat	gtc	547	
Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys	Thr	Asn	Pro	Asp	Val		
						140							145				
act	gga	cct	tca	cca	agt	ggc	att	ttg	cct	gct	act	ggc	tct	gtc	gcc	595	
Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala	Thr	Gly	Ser	Val	Ala		
						155							160				
gca	ctt	att	acc	gca	gct	act	ggc	gct	gag	cct	tat	tac	atc	ggc	aag	643	
Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro	Tyr	Tyr	Ile	Gly	Lys		
						170									180		
cca	aac	cct	gtg	atg	atg	cgc	agt	gcg	ctg	aac	acc	atc	ggg	gcg	cat	691	
Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn	Thr	Ile	Gly	Ala	His		
						185									195		
tcc	gag	cac	act	gtc	atg	atc	ggc	gac	cgc	atg	gac	acc	gac	gtg	aaa	739	
Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met	Asp	Thr	Asp	Val	Lys		
								205							210		
tct	ggg	ttg	gaa	ggc	ggc	ctg	agc	acc	gtg	ctg	gtt	cga	agc	gga	att	787	
Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu	Val	Arg	Ser	Gly	Ile		
								220							225		
tcc	gac	gac	ggc	gag	atc	cgc	cgc	tac	ccc	ttc	cgc	cca	act	cac	gtg	835	
Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe	Arg	Pro	Thr	His	Val		
																245	
atc	aat	tcc	atc	ggc	gat	ctt	ggc	gat	tgc	tgg	gac	gat	cct	ttc	ggg	883	
Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp	Asp	Asp	Pro	Phe	Gly		
																260	
gac	ggg	gca	ttt	cac	gta	cca	gat	gag	cag	cag	ttc	act	gac			925	
Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln	Phe	Thr	Asp				
																275	

tagtattctg taggtcatgg cat

948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met	Thr	Val	Asn	Ile	Ser	Tyr	Leu	Thr	Asp	Met	Asp	Gly	Val	Leu	Ile
1				5					10					15	

Lys	Glu	Gly	Glu	Ile	Ile	Pro	Gly	Ala	Asp	Arg	Phe	Leu	Gln	Ser	Leu
			20					25					30		

Thr	Asp	Asn	Asn	Val	Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe
		35					40					45			

Thr	Pro	Arg	Asp	Leu	Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile
	50					55					60				

Pro	Pro	Glu	Arg	Ile	Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu
65					70				75						80

Lys	Ser	Gln	Val	Lys	Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly
				85					90					95	

Leu	Thr	Thr	Ala	Leu	His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn
			100					105					110		

Pro	Glu	Phe	Val	Val	Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala
		115					120					125			

Ile	Thr	Thr	Ala	Ile	Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys
	130					135					140				

Thr	Asn	Pro	Asp	Val	Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala
145					150					155					160

Thr	Gly	Ser	Val	Ala	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro
			165						170					175	

Tyr	Tyr	Ile	Gly	Lys	Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn
			180					185					190		

Thr	Ile	Gly	Ala	His	Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met
	195						200					205			

Asp	Thr	Asp	Val	Lys	Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu
	210					215					220				

Val	Arg	Ser	Gly	Ile	Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe
225					230					235					240

Arg	Pro	Thr	His	Val	Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp
			245						250					255	

Asp	Asp	Pro	Phe	Gly	Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln
			260					265					270		

Phe Thr Asp
275

<210> 163
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> FRXA01468

<400> 163
tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115
Met Thr Val Asn Ile
1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
25 30 35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
40 45 50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
55 60 65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70 75 80 85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
90 95 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
105 110 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
120 125 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
135 140 145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150 155 160 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180

cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195

tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210

tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225

tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245

atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260

gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275

tagtattctg taggtcatgg cat 948

<210> 164

<211> 275

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
 275

<210> 165
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA00794

<400> 165
 gcgggttgat acagcccaag cgccgataca ttataatgc gcctagatac gtgcaaccca 60

cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
 Met Asn Leu Lys Asn
 1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
 10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
 25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
 40 45 50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
55						60					65						
gaa	gct	cca	atg	ctg	tac	aac	ggc	gaa	gag	gtc	gga	acc	ggc	ttt	gga	355	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
70					75					80					85		
cct	gag	gtt	gat	atc	gca	gtt	gac	cca	gtt	gac	ggc	acc	acc	ctg	atg	403	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95					100			
gct	gag	ggt	cgc	ccc	aac	gca	att	tcc	att	ctc	gca	gct	gca	gag	cgt	451	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Glu	Arg		
			105					110					115				
ggc	acc	atg	tac	gat	cca	tcc	tcc	gtc	ttc	tac	atg	aag	aag	atc	gcc	499	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
		120					125					130					
gtg	gga	cct	gag	gcc	gca	ggc	aag	atc	gac	atc	gaa	gct	cca	gtt	gcc	547	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
	135					140					145						
cac	aac	atc	aac	gcg	gtg	gca	aag	tcc	aag	gga	atc	aac	cct	tcc	gac	595	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
150					155					160					165		
gtc	acc	gtt	gtc	gtg	ctt	gac	cgt	cct	cgc	cac	atc	gaa	ctg	atc	gca	643	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac	att	cgt	cgt	gca	ggc	gca	aag	gtt	cgt	ctc	atc	tcc	gac	ggc	gac	691	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt	gca	ggt	gca	gtt	gca	gca	gct	cag	gat	tcc	aac	tcc	gtg	gac	atc	739	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
		200					205					210					
atg	atg	ggc	acc	ggc	gga	acc	cca	gaa	ggc	atc	atc	act	gcg	tgc	gcc	787	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
	215					220					225						
atg	aag	tgc	atg	ggt	ggc	gaa	atc	cag	ggc	atc	ctg	gcc	cca	atg	aac	835	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
230					235					240					245		
gat	ttc	gag	cgc	cag	aag	gca	cac	gac	gct	ggt	ctg	gtt	ctt	gat	cag	883	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255					260			
gtt	ctg	cac	acc	aac	gat	ctg	gtg	agc	tcc	gac	aac	tgc	tac	ttc	gtg	931	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
			265					270					275				
gca	acc	ggt	gtg	acc	aac	ggt	gac	atg	ctc	cgt	ggc	gtt	tcc	tac	cgc	979	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
		280					285					290					
gca	aac	ggc	gca	acc	acc	cgt	tcc	ctg	gtt	atg	cgc	gca	aag	tca	ggc	1027	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295 300 305
 acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
 310 315 320 325

 tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335

 aac 1128

 <210> 166
 <211> 335
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 166
 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
 1 5 10 15

 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
 20 25 30

 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
 35 40 45

 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
 50 55 60

 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
 65 70 75 80

 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
 85 90 95

 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
 100 105 110

 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
 115 120 125

 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
 130 135 140

 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
 145 150 155 160

 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
 165 170 175

 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
 180 185 190

 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
 195 200 205

 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
 210 215 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
 225 230 235 240
 Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
 245 250 255
 Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
 260 265 270
 Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
 275 280 285
 Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
 290 295 300
 Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
 305 310 315 320
 Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 325 330 335

<210> 167

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXN02920

<400> 167

tgcatgcaga ttatctgtcc aactacgccca gccgcgcgta aagcgcgggc ctgctggtgg 60

cgggtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg 115
 Met Lys Phe Val Met
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

90	95	100	
gcg acg act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa			451
Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu			
105	110	115	
aac aac aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc			499
Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly			
120	125	130	
gdc ggt ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac			547
Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn			
135	140	145	
gtg aag acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca			595
Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala			
150	155	160	165
gat gaa acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct			643
Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala			
170	175	180	
gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc			691
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile			
185	190	195	
gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc			739
Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val			
200	205	210	
aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca			787
Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala			
215	220	225	
ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct			835
Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro			
230	235	240	245
gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt			883
Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val			
250	255	260	
atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc			931
Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr			
265	270	275	
ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag			979
Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln			
280	285	290	
atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat			1032
Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr			
295	300		
ccg			1035

<210> 168

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

```

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
 1           5           10           15

Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
      20           25           30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
      35           40           45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
      50           55           60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
      65           70           75           80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
      85           90           95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
      100           105           110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
      115           120           125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
      130           135           140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
      145           150           155           160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
      165           170           175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
      180           185           190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
      195           200           205

Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
      210           215           220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
      225           230           235           240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
      245           250           255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
      260           265           270

Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
      275           280           285

Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
      290           295           300

```



```
<210> 169
<211> 779
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (52) .. (756)
<223> FRXA02379
```

<400> 169															
tgcaggcctc catggcgggt attgatgcgc tggatcaagcg tgggtgtcgtc aatg aga															57
Met Arg															
1															
aag cac cgt tgg gca aac gcg gct ggc ctg tac gct gac acc gtt gct	105														
Lys His Arg Trp Ala Asn Ala Gly Leu Tyr Ala Asp Thr Val Ala															
5 10 15															
gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat gcg acg	153														
Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His Ala Thr															
20 25 30															
act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa aac aac	201														
Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu Asn Asn															
35 40 45 50															
aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc gcc ggt	249														
Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly Ala Gly															
55 60 65															
ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac gtg aag	297														
Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn Val Lys															
70 75 80															
acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca gat gaa	345														
Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala Asp Glu															
85 90 95															
acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct gat gtg	393														
Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala Asp Val															
100 105 110															
ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc gtc aat	441														
Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile Val Asn															
115 120 125 130															
gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc aat gtg	489														
Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val Asn Val															
135 140 145															
ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca ttg aac	537														
Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala Leu Asn															
150 155 160															
aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct gag cca	585														
Asn Gly Thr Ile Ala Gly Ala Leu Asp Val Thr Asp Pro Glu Pro															
165 170 175															

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
 180 185 190

cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
 195 200 205 210

ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
 215 220 225

acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776
 Thr Glu Val Asp Val Val Ala Gly Tyr
 230 235

ccg 779

<210> 170

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 1 5 10 15

Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
 20 25 30

Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45

Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60

Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80

Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95

Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110

Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125

Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140

Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160

Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175

Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205

Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220

Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXN02688

<400> 171

gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115
 Met Ala Gly Arg Ile
 1 5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135 140 145
 atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc 595
 Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
 150 155 160 165
 agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg 643
 Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
 170 175 180
 gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
 Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
 185 190 195
 gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc 739
 Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
 200 205 210
 tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg 789
 Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
 215 220
 gat 792

 <210> 172
 <211> 223
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 172
 Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
 1 5 10 15
 Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
 20 25 30
 Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
 35 40 45
 Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
 50 55 60
 Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65 70 75 80
 Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
 85 90 95
 Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
 100 105 110
 Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
 115 120 125
 Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
 130 135 140
 Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
 145 150 155 160

<400> 174
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
1 5 10 15
Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr

20 25 30

Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
35 40 45

Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
50 55 60

Leu Glu Leu Glu Ala Lys Asn
65 70

<210> 175
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> RXN03186

<400> 175
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
55 60 65

cgc 310
Arg
70

<210> 176
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
1 5 10 15
Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg
 65 70

<210> 177

<211> 302

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

ggt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

caagggacag ata 302

<210> 178

<211> 93

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 178

Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

<400> 179																	
atgtgtccgt tgtctcacct aaagttttta ctagttctgt atctgaaagc tacgctaggg																	60
ggcgagaact ctgtcgaatg acacaaaatc tggagaagta																	
										atg	act	act	gct	gca			115
										Met	Thr	Thr	Ala	Ala			
										1				5			
atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg																	163
Ile	Arg	Gly	Leu	Gln	Gly	Glu	Ala	Pro	Thr	Lys	Asn	Lys	Glu	Leu	Leu		
				10					15					20			
aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg																	211
Asn	Trp	Ile	Ala	Asp	Ala	Val	Glu	Leu	Phe	Gln	Pro	Glu	Ala	Val	Val		
			25					30					35				
ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt																	259
Phe	Val	Asp	Gly	Ser	Gln	Ala	Glu	Trp	Asp	Arg	Met	Ala	Glu	Asp	Leu		
		40					45					50					
gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac																	307
Val	Glu	Ala	Gly	Thr	Leu	Ile	Lys	Leu	Asn	Glu	Glu	Lys	Arg	Pro	Asn		
	55					60					65						
agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc																	355
Ser	Tyr	Leu	Ala	Arg	Ser	Asn	Pro	Ser	Asp	Val	Ala	Arg	Val	Glu	Ser		
	70					75				80					85		
cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac																	403
Arg	Thr	Phe	Ile	Cys	Ser	Glu	Lys	Glu	Asp	Ala	Gly	Pro	Thr	Asn			
				90					95				100				
aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac																	451
Asn	Trp	Ala	Pro	Pro	Gln	Ala	Met	Lys	Asp	Glu	Met	Ser	Lys	His	Tyr		
			105					110					115				
gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg																	499
Ala	Gly	Ser	Met	Lys	Gly	Arg	Thr	Met	Tyr	Val	Val	Pro	Phe	Cys	Met		
		120				125						130					

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt	1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg	
375 380 385	
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac	1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn	
390 395 400 405	
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc	1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg	
410 415 420	
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc	1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly	
425 430 435	
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca	1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala	
440 445 450	
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca	1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro	
455 460 465	
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg	1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met	
470 475 480 485	
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg	1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp	
490 495 500	
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac	1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp	
505 510 515	
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt	1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val	
520 525 530	
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc	1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu	
535 540 545	
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg	1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu	
550 555 560 565	
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag	1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu	
570 575 580	
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag	1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln	
585 590 595	
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagtccac	1940
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala	
600 605 610	
gcttaagaac tgc	1953

<210> 180

<211> 610

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 180

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
 1 5 10 15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
 20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
 260 265 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
 275 280 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
 325 330 335
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
 340 345 350
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
 355 360 365
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
 370 375 380
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
 385 390 395 400
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
 405 410 415
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
 420 425 430
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
 435 440 445
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
 450 455 460
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
 465 470 475 480
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
 485 490 495
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
 500 505 510
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
 515 520 525
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
 530 535 540
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
 545 550 555 560
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
 565 570 575
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
 580 585 590
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
 595 600 605

His Ala
610

<210> 181
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXS01260

<400> 181
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccatatc 60

ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
Val Thr Phe Asn Tyr
1 5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
10 15 20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
25 30 35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
40 45 50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
55 60 65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70 75 80 85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
90 95 100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
105 110 115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
120 125 130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
135 140 145

aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctg atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctg acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctgcttggcc ctg	1305
His Met Ile Asn Phe	
390	

<210> 182

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
 1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
 20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
 35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
 50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
 65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
 85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
 100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
 115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
 130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
 145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
 165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
 180 185 190

Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
 195 200 205

Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
 210 215 220

Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
 225 230 235 240

Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
 245 250 255

Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
 260 265 270

Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
 275 280 285

Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val

290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
385 390

<210> 183
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXS01261

<400> 183
gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60
atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
Val Thr Glu His Tyr
1 5
gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
10 15 20
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
25 30 35
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
40 45 50
gat caa aaa cgc tgaagttgcc cataccttta ccc 294
Asp Gln Lys Arg
55

```
<210> 184
<211> 57
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 184

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 185
 <211> 1650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXA02640

<400> 185
 accaacgcacg acgccggtgt agcagatgta ttggagtggg ggttctaata ggtgggtgtta 60
 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
 Met Arg Ile Ser Lys
 1 5
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
 10 15 20
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
 25 30 35
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
 40 45 50
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
 55 60 65
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
 70 75 80 85
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
 90 95 100
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
 120 125 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
 375 380 385
 cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
 390 395 400 405
 gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
 410 415 420
 ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
 425 430 435
 ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
 440 445 450
 ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
 455 460 465
 gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
 470 475 480 485
 atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500
 gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
 Val Glu His Ser Tyr Asp Gln Ala
 505

<210> 186

<211> 509

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 186

Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly
 1 5 10 15
 Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val
 20 25 30
 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
 35 40 45
 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
 50 55 60
 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65 70 75 80
 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
 85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 245 250 255
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 260 265 270
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 275 280 285
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 290 295 300
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 305 310 315 320
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 325 330 335
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 340 345 350
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 355 360 365
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 370 375 380
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
 385 390 395 400
 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
 405 410 415
 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

420	425	430	
Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val			
435	440	445	
Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly			
450	455	460	
Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys			
465	470	475	480
Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala			
485	490	495	
Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala			
500	505		
<210> 187			
<211> 1119			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1096)			
<223> RXN01025			
<400> 187			
gggcagcagc ggcaggtttc caggaggttt ccatgcgggt ggcttgggac atgggctaac 60			
ctgagacggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115			
		Val Val Ser Val Ser	
		1 5	
gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163			
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser			
10	15	20	
gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211			
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala			
25	30	35	
agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259			
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile			
40	45	50	
acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307			
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu			
55	60	65	
gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355			
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg			
70	75	80	85
ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403			
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu			
90	95	100	
gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451			
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser			

105						110						115						
gaa	gtg	atc	gcg	gag	gtg	acg	gaa	gcg	gat	cct	tca	cgc	atc	gcg	gtg	499		
Glu	Val	Ile	Ala	Glu	Val	Thr	Glu	Ala	Asp	Pro	Ser	Arg	Ile	Ala	Val			
120						125						130						
ttg	tcg	ggg	cca	aac	ctt	gct	cgt	gag	atc	gcg	gag	ggg	cag	cct	gca	547		
Leu	Ser	Gly	Pro	Asn	Leu	Ala	Arg	Glu	Ile	Ala	Glu	Gly	Gln	Pro	Ala			
135						140						145						
gct	acg	gtg	att	gct	tgc	cct	gat	gaa	aac	cga	gcg	aaa	ctt	gtg	cag	595		
Ala	Thr	Val	Ile	Ala	Cys	Pro	Asp	Glu	Asn	Arg	Ala	Lys	Leu	Val	Gln			
150						155						160						165
gct	gca	gtg	gct	gcg	ccg	tat	ttc	cgc	ccg	tac	acc	aac	act	gat	gtg	643		
Ala	Ala	Val	Ala	Ala	Pro	Tyr	Phe	Arg	Pro	Tyr	Thr	Asn	Thr	Asp	Val			
170						175						180						
gtg	ggc	act	gaa	atc	ggt	ggt	gcg	tgt	aag	aac	gtc	atc	gcg	ctg	gcc	691		
Val	Gly	Thr	Glu	Ile	Gly	Gly	Ala	Cys	Lys	Asn	Val	Ile	Ala	Leu	Ala			
185						190						195						
tgt	ggt	att	tcc	cat	ggt	tac	ggc	ctg	ggt	gag	aac	acc	aat	gca	tcg	739		
Cys	Gly	Ile	Ser	His	Gly	Tyr	Gly	Leu	Gly	Glu	Asn	Thr	Asn	Ala	Ser			
200						205						210						
ttg	att	act	cgt	ggc	ctt	gca	gag	atc	gca	cgc	ctc	ggt	gcc	aca	ttg	787		
Leu	Ile	Thr	Arg	Gly	Leu	Ala	Glu	Ile	Ala	Arg	Leu	Gly	Ala	Thr	Leu			
215						220						225						
ggt	gcg	gat	gcg	aag	act	ttt	tct	ggc	ctt	gcg	gga	atg	ggc	gac	ttg	835		
Gly	Ala	Asp	Ala	Lys	Thr	Phe	Ser	Gly	Leu	Ala	Gly	Met	Gly	Asp	Leu			
230						235						240						245
gtg	gct	acg	tgt	tca	tca	ccg	ctg	tcg	cgt	aac	cgc	agc	ttc	ggt	gag	883		
Val	Ala	Thr	Cys	Ser	Ser	Pro	Leu	Ser	Arg	Asn	Arg	Ser	Phe	Gly	Glu			
250						255						260						
cgt	ttg	ggt	cag	ggt	gaa	tcc	cta	gag	aag	gct	cgc	gag	gca	acc	aat	931		
Arg	Leu	Gly	Gln	Gly	Glu	Ser	Leu	Glu	Lys	Ala	Arg	Glu	Ala	Thr	Asn			
265						270						275						
ggt	cag	gtt	gcg	gag	ggt	gtt	att	tcc	tcg	cag	tcg	att	ttt	gat	ctt	979		
Gly	Gln	Val	Ala	Glu	Gly	Val	Ile	Ser	Ser	Gln	Ser	Ile	Phe	Asp	Leu			
280						285						290						
gcc	acc	aag	ctt	ggt	gtg	gag	atg	ccg	atc	acc	cag	gct	gtc	tac	ggt	1027		
Ala	Thr	Lys	Leu	Gly	Val	Glu	Met	Pro	Ile	Thr	Gln	Ala	Val	Tyr	Gly			
295						300						305						
gtg	tgc	cac	cga	gat	atg	aaa	gta	act	gac	atg	att	gtg	gct	ctc	atg	1075		
Val	Cys	His	Arg	Asp	Met	Lys	Val	Thr	Asp	Met	Ile	Val	Ala	Leu	Met			
310						315						320						325
ggc	agg	tct	aag	aag	gct	gag	tagtcttagg	ttgtaagctt	caa							1119		
Gly	Arg	Ser	Lys	Lys	Ala	Glu												
330																		

<210> 188

<211> 332

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 188

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
 1 5 10 15
 Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
325 330

<210> 189

<211> 1015

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> FRXA01025

<400> 189

gggcagcagc ggcagggtttc cagraggttt ccatgcgggt ggcttggrac wtgggctaac 60

ctgaracggt taaatatcgt ttctgaaagg tgggtttcgc gtg gtt tct gta agc 115
Val Val Ser Val Ser
1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg ccg atg agt 451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
135 140 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
 150 155 160 165
 gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
 Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
 170 175 180
 gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
 Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
 185 190 195
 tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
 Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
 200 205 210
 ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
 Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
 215 220 225
 ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg 835
 Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
 230 235 240 245
 gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag 883
 Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
 250 255 260
 cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat 931
 Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
 265 270 275
 ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
 280 285 290
 gcc acc aag ctt ggt gtg gag atg ccg atc acc cag 1015
 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln
 295 300 305
 <210> 190
 <211> 305
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 190
 Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
 1 5 10 15
 Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300
 Gln
 305

<210> 191
 <211> 1809
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1786)
 <223> RXA01851

<400> 191
 ttgtggcctt tttgcagggg aaacttattt aaataattca taagtaaaaa accgtcaatt 60
 cacgatgtgg gttggcggtt ttctatttag gctcactttt atg acg agc gca cac 115
 Met Thr Ser Ala His

	1	5	
ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc	163		
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val			
10 15 20			
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct	211		
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala			
25 30 35			
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct	259		
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser			
40 45 50			
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc	307		
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg			
55 60 65			
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa	355		
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu			
70 75 80 85			
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt	403		
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser			
90 95 100			
ttc atg ctc acg cgc ttt gat tgg tca gag ccg aaa gcc cct atg ttg	451		
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu			
105 110 115			
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag	499		
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln			
120 125 130			
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa	547		
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys			
135 140 145			
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag	595		
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys			
150 155 160 165			
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc	643		
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu			
170 175 180			
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc	691		
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile			
185 190 195			
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc	739		
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg			
200 205 210			
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag	787		
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu			
215 220 225			
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag	835		
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln			
230 235 240 245			

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc	883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser	
250 255 260	
aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg	931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val	
265 270 275	
ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg	979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met	
280 285 290	
ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct	1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala	
295 300 305	
gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc	1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr	
310 315 320 325	
atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc	1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser	
330 335 340	
acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac	1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr	
345 350 355	
acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att	1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile	
360 365 370	
gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg	1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val	
375 380 385	
atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg	1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val	
390 395 400 405	
tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act	1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr	
410 415 420	
tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt	1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu	
425 430 435	
cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg	1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu	
440 445 450	
gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca	1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala	
455 460 465	
aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc	1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile	
470 475 480 485	

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

tcacgcacac cgg 1809

<210> 192
 <211> 562
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
 Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
 1 5 10 15

Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
 165 170 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
 180 185 190
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
 195 200 205
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
 210 215 220
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
 225 230 235 240
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
 245 250 255
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
 260 265 270
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
 275 280 285
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
 290 295 300
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
 305 310 315 320
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495

Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly
 500 505 510

Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala
 515 520 525

Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys
 530 535 540

Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro
 545 550 555 560

Tyr Arg

<210> 193
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(877)
 <223> RXA01242

<400> 193
 cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatatatta gtaaattggc tttttgcttt aaggagtgc atg tac gca gag gag 115
 Met Tyr Ala Glu Glu
 1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
 10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
 25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
 Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
 40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
 55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355
 Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
 90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
 105 110 115

```

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
      120                      125                      130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
      135                      140                      145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
      150                      155                      160

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
      170                      175                      180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
      185                      190                      195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
      200                      205                      210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
      215                      220                      225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
      230                      235                      240                      245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
      250                      255

tgattcttac agtcactgca agt 900

```

<210> 194

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 194

```

Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
  1              5              10              15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
      20              25              30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
      35              40              45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
      50              55              60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
      65              70              75              80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

```


85										90					95				
Gly	Leu	Phe	Leu	Asp	Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu				
			100						105					110					
Ile	Ser	Glu	His	Pro	Ser	Ser	Lys	Gln	Trp	Ser	Ile	Val	Thr	Asn	Cys				
		115					120					125							
Leu	Pro	Ile	Ala	Leu	Asn	Leu	Ala	Asn	Ala	Gly	Leu	Asp	Asp	Val	Gln				
	130					135					140								
Leu	Leu	Gly	Gly	Ser	Val	Arg	Ala	Ile	Thr	Gln	Ala	Val	Val	Gly	Asp				
145					150					155					160				
Thr	Ala	Leu	Arg	Thr	Leu	Ala	Leu	Met	Arg	Ala	Asp	Val	Val	Phe	Ile				
				165					170					175					
Gly	Thr	Asn	Ala	Leu	Thr	Leu	Asp	His	Gly	Leu	Ser	Thr	Ala	Asp	Ser				
		180						185					190						
Gln	Glu	Ala	Ala	Met	Lys	Ser	Ala	Met	Ile	Thr	Asn	Ala	His	Lys	Val				
	195						200					205							
Val	Val	Leu	Cys	Asp	Ser	Thr	Lys	Met	Gly	Thr	Asp	Tyr	Leu	Val	Ser				
	210					215					220								
Phe	Gly	Ala	Ile	Ser	Asp	Ile	Asp	Val	Val	Val	Thr	Asp	Ala	Gly	Ala				
225					230					235					240				
Pro	Ala	Ser	Phe	Val	Glu	Gln	Leu	Arg	Glu	Arg	Asp	Val	Glu	Val	Val				
			245					250					255						

Ile Ala Glu

<210> 195

<211> 969

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(946)

<223> RXA02288

<400> 195

aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatgtagaa 60

agtgc	tggat	ctaaca	acat	ttccgt	ggta	acttttt	cac	atg	tcc	caa	gtg	att	115
								Met	Ser	Gln	Val	Ile	
								1				5	

ccc	gcc	agc	tca	caa	gaa	aag	cgt	cgt	gag	cgc	atc	gtt	tct	tat	gtc	163
Pro	Ala	Ser	Ser	Gln	Glu	Lys	Arg	Arg	Glu	Arg	Ile	Val	Ser	Tyr	Val	
				10					15					20		

acc	cgt	cat	gga	ttc	gct	cgt	gtt	gaa	gca	tta	gct	gag	ctt	ttt	gag	211
Thr	Arg	His	Gly	Phe	Ala	Arg	Val	Glu	Ala	Leu	Ala	Glu	Leu	Phe	Glu	
			25					30						35		

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp	
40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser	
55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val	
70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala	
90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys	
105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr	
120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile	
135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys	
150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val	
170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His	
185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly	
200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly	
215 220 225	
gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat	835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp	
230 235 240 245	
cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg	883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala	
250 255 260	
cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca	931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro	
265 270 275	
acg gaa gag gat ttt taagatggct ttggttcttg gaa	969

Thr Glu Glu Asp Phe
280

<210> 196

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
1 5 10 15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 197
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> RXN01891

<400> 197
ggt ggc cac tat ggt ttg cct ttc gct cgc tcc act gtc ctc ttc tac 48
Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
1 5 10 15
tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30
gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45
atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60
tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80
gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95
gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110
gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125
tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg 432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
130 135 140
ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160
ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
165 170 175
gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act 576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr

180					185					190					
ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct	624														
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala															
195 200 205															
gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac	672														
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr															
210 215 220															
aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc	720														
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe															
225 230 235 240															
cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag	768														
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu															
245 250 255															
aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt	816														
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val															
260 265 270															
gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att	864														
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile															
275 280 285															
taatccgagc acttcagcta cac	887														

<210> 198

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
 1 5 10 15

Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
 20 25 30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
 35 40 45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
 50 55 60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
 65 70 75 80

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
 85 90 95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
 100 105 110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
 115 120 125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
 130 135 140

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
 145 150 155 160
 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
 165 170 175
 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
 180 185 190
 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
 195 200 205
 Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
 210 215 220
 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
 225 230 235 240
 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
 245 250 255
 Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
 260 265 270
 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
 275 280 285

<210> 199
 <211> 842
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(819)
 <223> FRXA01891

<400> 199
 tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc 48
 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

65	70	75	80	
gtt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc				288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tct gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
gtt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

<210> 200

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
 180 185 190
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
 195 200 205
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
 210 215 220
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
 225 230 235 240
 Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
 245 250 255
 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
 260 265 270
 Ile

<210> 201

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

tttaccatg agt tac aac agc ccg tat aac aac acg aat ttc agc acc act 51

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
1 5 10 15

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99

Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
20 25 30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147

Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
35 40 45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195

Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
50 55 60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243

Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
65 70 75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291

Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
80 85 90 95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339

Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
100 105 110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387

Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
115 120 125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435

Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
130 135 140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483

Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
145 150 155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531

Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
160 165 170 175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579

Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
180 185 190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627

Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
195 200 205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675

Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
210 215 220

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagcgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
 1 5 10 15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
 65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
 85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
 100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
 115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
 130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
 145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
 165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
 180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
 195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
 210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
 225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

<210> 203

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN01580

<400> 203

cggtaaacgc ctcattaaag tccaatgcc a tgctcataac actaacagtt aaccgtgcgg 60

tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
Met Tyr Lys Asn Met
1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
10 15 20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
25 30 35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
40 45 50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
55 60 65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70 75 80 85

tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
90 95 100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala
105 110 115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
120 125 130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
135 140 145

cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150 155 160 165

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643
 Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
 170 175 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691
 Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
 185 190 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739
 Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
 200 205 210

caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787
 Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
 215 220 225

gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837
 Ala Pro Ser Pro Ala Gly Glu Leu His Trp
 230 235

ctg 840

<210> 204

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
 1 5 10 15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
 20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
 35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
 50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
 85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
 100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
 115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
 130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

	165		170		175	
Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His	180		185		190	
Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala	195		200		205	
Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp	210		215		220	
Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp	225		230		235	

<210> 205
 <211> 1314
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(1291)
 <223> RXA01436
 <400> 205.

```

gcctaaacaa accagtcaac gacctttccc gtggcgcaac agtccttgac atcgtaaca 60
cagtagccat cacagcaatt caggcaggag gacgcagcta atg gca ttg gca ctt 115
                                     Met Ala Leu Ala Leu
                                     1           5

gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc 163
Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro
                10                15                20

gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag 211
Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln
                25                30                35

att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa 259
Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys
                40                45                50

tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg 307
Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu
                55                60                65

gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa 355
Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu
                70                75                80                85

atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc 403
Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser
                90                95                100

gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc 451
Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu
                105                110                115

att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat 499
  
```

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp		
		120					125					130					
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547	
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp		
		135				140					145						
acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595	
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile		
		150			155					160					165		
aac	aag	gat	gtc	gca	gct	gaa	cac	gga	atc	agg	cgc	tat	ggt	ttc	cac	643	
Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His		
				170				175						180			
ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691	
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu		
			185					190					195				
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739	
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly		
		200					205					210					
gca	tcc	atg	gct	gct	gtt	caa	ggg	ggc	cgt	gcg	gta	gat	act	tcc	atg	787	
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met		
		215				220					225						
ggg	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggg	acc	cga	agc	ggg	gac	835	
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp		
		230			235				240						245		
att	gat	cca	ggg	atc	gtc	ttc	cac	ctt	tcc	cgc	acc	gct	ggc	atg	agc	883	
Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser		
				250					255					260			
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tcg	ggg	gta	aag	gga	931	
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly		
			265					270					275				
ctt	tcc	ggg	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979	
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn		
		280					285					290					
aat	gat	caa	gat	gcc	ttg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027	
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu		
		295				300					305						
cgc	cgc	tac	ctc	ggg	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075	
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr		
		310			315					320					325		
atc	gtg	ttc	acc	gcc	ggg	gtc	ggg	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123	
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu		
				330					335					340			
gat	gcc	ttg	gca	ggg	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171	
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu		
			345					350					355				
cgt	aac	gca	ttg	cca	aac	gat	ggg	cct	cga	ttg	att	tcc	acc	gat	gcc	1219	
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala		

360 365 370
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385

gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

<210> 206

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
 1 5 10 15

Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
 20 25 30

Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45

Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60

Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65 70 75 80

Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
 85 90 95

Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
 100 105 110

Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
 115 120 125

Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
 130 135 140

Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
 145 150 155 160

Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
 165 170 175

Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
 180 185 190

Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
 195 200 205

His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
 210 215 220

Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
 225 230 235 240

Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg
245 250 255

Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys
260 265 270

Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg
275 280 285

Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile
290 295 300

Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu
305 310 315 320

Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala
325 330 335

Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile
340 345 350

Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu
355 360 365

Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn
370 375 380

Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
385 390 395

<210> 207

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00686

<400> 207

ataggcttga acaatacgtc gttacactgg ccgatttgat acctttcaaa actttttaccc 60

ttcatcgagg tgccagggga acttagagga gcattaaata atg gcg gga gga aat 115
Met Ala Gly Gly Asn
1 5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
40 45 50


```

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
    55                60                65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
    70                75                80                85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
    90                95                100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
    105                110                115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
    120                125                130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
    135                140                145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
    150                155                160                165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
    170                175                180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
    185                190                195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
    200                205                210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
    215                220                225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
    230                235                240                245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
    250                255                260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata 927
Ala Glu Arg Lys Gly Asp Thr
    265

```

<210> 208

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

```

Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
 1           5           10           15

Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
      20           25           30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
      35           40           45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
      50           55           60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
      65           70           75           80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
      85           90           95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
      100          105          110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
      115          120          125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
      130          135          140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
      145          150          155          160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
      165          170          175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
      180          185          190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
      195          200          205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
      210          215          220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
      225          230          235          240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
      245          250          255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
      260          265

```

<210> 209

<211> 1158

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1135)

<223> RXA00246

<400> 209

ttgcaaggat tgtaatttaa ggcacatcta tgtcgggtgtg aaattacatg tgccagaaga 60

gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115
 Met Thr Thr Ala Ala
 1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
 Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
 10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
 Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
 25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
 Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
 40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
 Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
 55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
 Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
 70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
 Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
 90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
 Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
 105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
 Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
 120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
 Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
 135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
 Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
 150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
 Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
 170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
 Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Met Gly Met
 185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739
 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
 200 205 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787
Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
215 220 225

gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
230 235 240 245

act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
250 255 260

cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
265 270 275

gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
280 285 290

ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
295 300 305

cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
310 315 320 325

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
330 335 340

gcg att cgt ttc taacggattg tgttgaaact gct 1158
Ala Ile Arg Phe
345

<210> 210

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
1 5 10 15

Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
20 25 30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
35 40 45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
50 55 60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
65 70 75 80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
 245 250 255
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
 260 265 270
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
 275 280 285
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
 290 295 300
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
 305 310 315 320
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
 325 330 335
 Ile Asp Gly Arg Val Ala Ile Arg Phe
 340 345

<210> 211

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01571

<400> 211

```

aaactacctg ctgagagctt tgtaatttac ggtgtggttg tggaggggtg cgtcgagaag 60
cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta 115
                               Val Ser Ile Ser Val
                               1 5

aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
                               10 15 20

att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211
Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
                               25 30 35

gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
                               40 45 50

ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
                               55 60 65

gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
                               70 75 80 85

gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
                               90 95 100

gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac 451
Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
                               105 110 115

aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa 499
Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
                               120 125 130

aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt 547
Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
                               135 140 145

aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac 595
Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
                               150 155 160 165

tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc 643
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
                               170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
                               185 190 195

caa ggg tgc tgaggttacc gttctgtccc gtt 723
Gln Gly Cys
                               200

```

<210> 212

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 213

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA01572

<400> 213

ctgctgtgcg caggcatcac cacctactcc ccaatcgctc gctggaacgt taaagaaggc 60

gacaaagtag cagtcattggg cctcggcggg actcggacac atg ggt gtc cag atc 115
 Met Gly Val Gln Ile
 1 5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
 10 15 20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160

taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
 1 5 10 15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160
 Val Glu Ala Val

<210> 215
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXA01758

<400> 215
 ccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60
 gatagcgcg tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
 55 60 65
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
 70 75 80 85
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

90								95				100					
gca Ala	ggt Gly	gat Asp	cct Pro 105	gtg Val	cat His	tgc Cys	aga Arg	gag Glu 110	cgg Arg	aag Lys	att Ile	cct Pro	ggc Gly 115	gtt Val	tct Ser	451	
tat Tyr	gcg Ala	ggt Gly 120	ggt Gly	tgg Trp	gca Ala	cag Gln 125	aat Asn	att Ile	gtt Val	gtt Val	cca Pro	gcg Ala 130	gag Glu	gct Ala	ctt Leu	499	
gct Ala	gcg Ala 135	att Ile	cca Pro	gat Asp	ggc Gly 140	atg Met	gac Asp	ttt Phe	tac Tyr	gag Glu 145	ccc Pro	gcc Ala 150	ccg Pro	atg Met	ggc Gly	547	
tgc Cys 150	gca Ala	ggt Gly	gtg Val	aca Thr 155	aca Thr 155	ttc Phe	aat Asn	gcg Ala	ttg Leu 160	cga Arg 160	aac Asn	ctg Leu	aag Lys	ctg Leu	gat Asp 165	595	
ccc Pro	ggt Gly	gcg Ala	gct Ala 170	gtc Val	gcg Ala	gtc Val	ttt Phe	gga Gly 175	atc Ile 175	ggc Gly	ggt Gly	tta Leu 180	gtg Val	cgc Arg 180	cta Leu	643	
gct Ala	att Ile	cag Gln 185	ttt Phe	gct Ala	gcg Ala	aaa Lys	atg Met	ggt Gly 190	tat Tyr	cga Arg	acc Thr	atc Ile 195	acc Thr	atc Ile	gcc Ala	691	
cgc Arg	ggt Gly 200	tta Leu	gag Glu	cgt Arg	gag Glu	gag Glu	cta Leu 205	gct Ala	agg Arg	caa Gln	ctt Leu 210	ggc Gly 210	gcc Ala	aac Asn	cac His	739	
tac Tyr	atc Ile 215	gat Asp	agc Ser	aat Asn	gat Asp	ctg Leu 220	cac His	cct Pro	ggc Gly	cag Gln	gcg Ala 225	tta Leu	ttt Phe	gaa Glu	ctt Leu	787	
ggc Gly 230	ggg Gly	gct Ala	gac Asp	ttg Leu	atc Ile 235	ttg Leu	tct Ser	act Thr	gcg Ala	tcc Ser 240	acc Thr	acg Thr	gag Glu	cct Pro	ctt Leu 245	835	
tcg Ser	gag Glu	ttg Leu	tct Ser	acc Thr 250	ggt Gly	ctt Leu	tct Ser	att Ile	ggc Gly 255	ggg Gly	cag Gln	cta Leu	acc Thr	att Ile 260	atc Ile	883	
gga Gly	gtt Val	gat Asp	ggg Gly 265	gga Gly	gat Asp	atc Ile	acc Thr	gtt Val 270	tcg Ser	gca Ala	gcc Ala	caa Gln	ttg Leu 275	atg Met	atg Met	931	
aac Asn	cgt Arg 280	cag Gln	atc Ile	atc Ile	aca Thr	ggt Gly	cac His 285	ctc Leu	act Thr	gga Gly	agt Ser	gcg Ala 290	aat Asn	gac Asp	acg Thr	979	
gaa Glu	cag Gln 295	act Thr	atg Met	aaa Lys	ttt Phe	gct Ala 300	cat His	ctc Leu	cat His	ggc Gly 305	gtg Val	aaa Lys	ccg Pro	ctt Leu	att Ile	1027	
gaa Glu 310	cgg Arg	atg Met	cct Pro	ctc Leu	gat Asp 315	caa Gln	gcc Ala	aac Asn	gag Glu	gct Ala 320	att Ile	gca Ala	cgt Arg	att Ile	tca Ser 325	1075	
gct Ala	ggt Gly	aaa Lys	cca Pro	cgt Arg 330	ttc Phe	cgt Arg	att Ile	gtc Val 335	ttg Leu	gag Glu	ccg Pro	aat Asn	tca Ser			1117	

taatgccaac agcaagccca att

1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met	Pro	Lys	Tyr	Ile	Ala	Met	Gln	Val	Ser	Glu	Ser	Gly	Ala	Pro	Leu
1				5					10					15	

Ala	Ala	Asn	Leu	Val	Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg
			20					25					30		

Val	Glu	Ile	Ala	Ala	Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala
		35					40					45			

Ala	Ala	Ser	Gly	Lys	His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu
	50					55					60				

Ile	Ala	Gly	Thr	Ile	Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr
65					70					75					80

Val	Gly	Asp	Arg	Val	Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp
				85					90					95	

Cys	Ala	Phe	Cys	Arg	Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys
			100					105					110		

Ile	Pro	Gly	Val	Ser	Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val
		115					120					125			

Pro	Ala	Glu	Ala	Leu	Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu
	130					135					140				

Pro	Ala	Pro	Met	Gly	Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg
145					150					155					160

Asn	Leu	Lys	Leu	Asp	Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly
				165					170					175	

Gly	Leu	Val	Arg	Leu	Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg
			180					185					190		

Thr	Ile	Thr	Ile	Ala	Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln
		195					200					205			

Leu	Gly	Ala	Asn	His	Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln
	210					215					220				

Ala	Leu	Phe	Glu	Leu	Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser
225					230					235					240

Thr	Thr	Glu	Pro	Leu	Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly
				245					250					255	

Gln	Leu	Thr	Ile	Ile	Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala
			260					265					270		

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 217
 <211> 1641
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1618)
 <223> RXA02539

<400> 217
 ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcggt gaccaagtgt cacctgacgc 60

acaggtagtg ctcagggtgga ggtggcccaa aggagaccca atg act gtc tac gca 115
 Met Thr Val Tyr Ala
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Val Glu Gly Gln Tyr Leu
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
 105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile	
120 125 130	
cg t gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala	
135 140 145	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
150 155 160 165	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
170 175 180	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser	
185 190 195	
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val	
200 205 210	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser	
215 220 225	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc	835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
230 235 240 245	
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
 360 365 370
 aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt 1267
 Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
 375 380 385
 ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga 1315
 Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
 390 395 400 405
 cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt 1363
 Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
 410 415 420
 att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt 1411
 Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
 425 430 435
 gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga 1459
 Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
 440 445 450
 gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt 1507
 Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
 455 460 465
 gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg 1555
 Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
 470 475 480 485
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500
 cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 218

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
 1 5 10 15
 Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
 20 25 30
 Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45
 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60
 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95
 Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110
 Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125
 Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140
 His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160
 Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175
 Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190
 Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205
 Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220
 Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240
 Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380
 Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
 385 390 395 400
 Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe

405	410	415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala		
420	425	430
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala		
435	440	445
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala		
450	455	460
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn		
465	470	480
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val		
485	490	495
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe		
500	505	

<210> 219

<211> 430

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN03061

<400> 219

ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60

gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa	gtg tct ttg acc ttc	115
	Val Ser Leu Thr Phe	
	1 5	

cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac	163
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn	
10 15 20	

cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct	211
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala	
25 30 35	

ggg cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc	259
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu	
40 45 50	

acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag	307
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu	
55 60 65	

atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa	355
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu	
70 75 80 85	

gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg	403
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val	
90 95 100	

cgc ctg ccc ggc cgc tac gga cag tca
 Arg Leu Pro Gly Arg Tyr Gly Gln Ser
 105 110

430

<210> 220

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
 1 5 10 15

Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
 20 25 30

Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
 35 40 45

Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
 50 55 60

Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
 65 70 75 80

Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
 85 90 95

Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
 100 105 110

<210> 221

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXN03150

<400> 221

tttaacagag tgcgtttcaa tgcctgtagt gttccggcaa ttttgaatgt cgttacggtt 60

accaaggct gaattcctga gtcaccttg tacaagatca gtg gaa gcc cag ttc 115
 Val Glu Ala Gln Phe
 1 5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
 Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
 10 15 20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
 Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
 25 30 35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
 Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr

```

          40          45          50
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc 307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
    55          60          65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc 355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
    70          75          80          85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg 403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
          90          95          100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc 451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
          105          110          115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc 499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
          120          125          130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg 547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
          135          140          145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga 595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly
          150          155          160          165

acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga 643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
          170          175          180

ggg gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt 691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
          185          190          195

gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
          200          205

tat 747

```

<210> 222

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

```

Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
  1          5          10          15

```

```

Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
  20          25          30

```

```

Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
  35          40          45

```

```

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg

```

50 55 60
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 223

<211> 881

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(858)

<223> RXN01340

<400> 223

aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg 48
 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15

cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30

gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45

tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60

ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp	
65 70 75 80	
gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa	288
Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys	
85 90 95	
ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt	336
Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Asn Arg Phe Leu Val	
100 105 110	
cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg	384
His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met	
115 120 125	
cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg	432
Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg	
130 135 140	
atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc	480
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile	
145 150 155 160	
atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc	528
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr	
165 170 175	
atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc	576
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile	
180 185 190	
ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc	624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly	
195 200 205	
gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc	672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe	
210 215 220	
agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc	720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala	
225 230 235 240	
gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct	768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro	
245 250 255	
ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa	816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu	
260 265 270	
gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg	858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro	
275 280 285	
tgacacatga gctgtccggt gaa	881

<210> 224

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175

Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190

Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255

Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270

Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285

<210> 225

<211> 1686

<212> DNA

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
260 265 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
275 280 285

Thr Gly Gly Thr Pro Thr Pro
290 295

<210> 317

<211> 1008

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(985)

<223> FRXA02654

<400> 317

tatttttcgga aatttataca gcaatcctcg aaatcctaataaagatccct tatcgtggga 60

gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
Met Ile Ser Leu Leu
1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
55 60 65

tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu	
70					75					80					85	

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
90 95 100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451
Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
120 125 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcggaaac act			1008
Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met	Ile	Ser	Leu	Leu	Asn	Asp	Pro	Arg	Thr	Leu	Phe	Pro	Lys	Val	Asp
1				5					10					15	

Pro	Pro	Lys	Gln	Ser	Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser
			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35					40					45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270
 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285
 Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 319
 <211> 1605
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1582)
 <223> RXN01049

<400> 319
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60

aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro

1														5		
aca	atg	tcc	atc	cct	ttt	gat	gac	tca	cgt	gga	cct	tat	gtc	ctt	gct	163
Thr	Met	Ser	Ile	Pro	Phe	Asp	Asp	Ser	Arg	Gly	Pro	Tyr	Val	Leu	Ala	
				10					15					20		
atg	gat	att	ggt	tcc	act	gca	tca	cga	ggt	gga	ctt	tat	gat	gct	tcc	211
Met	Asp	Ile	Gly	Ser	Thr	Ala	Ser	Arg	Gly	Gly	Leu	Tyr	Asp	Ala	Ser	
				25					30					35		
ggc	tgc	cca	atc	aaa	ggc	acc	aag	cag	cgc	gaa	tcc	cat	gaa	ttc	acc	259
Gly	Cys	Pro	Ile	Lys	Gly	Thr	Lys	Gln	Arg	Glu	Ser	His	Glu	Phe	Thr	
				40					45					50		
acc	ggt	gag	ggc	gtt	tcc	acc	att	gat	gct	gac	cag	gtg	gtt	tcg	gag	307
Thr	Gly	Glu	Gly	Val	Ser	Thr	Ile	Asp	Ala	Asp	Gln	Val	Val	Ser	Glu	
				55					60					65		
atc	acc	tca	gtt	att	aat	ggc	att	ttg	aac	gcg	gct	gat	cat	cac	aac	355
Ile	Thr	Ser	Val	Ile	Asn	Gly	Ile	Leu	Asn	Ala	Ala	Asp	His	His	Asn	
				70					75					80		
atc	aaa	gat	cag	atc	gcc	gct	gtc	gcg	cta	gat	tct	ttt	gca	tcc	tca	403
Ile	Lys	Asp	Gln	Ile	Ala	Ala	Val	Ala	Leu	Asp	Ser	Phe	Ala	Ser	Ser	
				90					95					100		
tta	atc	ttg	gtc	gat	ggt	gaa	ggc	aat	gcg	ctc	acc	ccg	tgc	att	acc	451
Leu	Ile	Leu	Val	Asp	Gly	Glu	Gly	Asn	Ala	Leu	Thr	Pro	Cys	Ile	Thr	
				105					110					115		
tac	gcg	gat	tct	cgt	tct	gca	cag	tat	gtg	gag	cag	ctg	cgc	gcg	gaa	499
Tyr	Ala	Asp	Ser	Arg	Ser	Ala	Gln	Tyr	Val	Glu	Gln	Leu	Arg	Ala	Glu	
				120					125					130		
atc	gat	gag	aag	gcc	tac	cac	ggc	cgc	acc	ggc	gtc	tgc	ttg	cac	acc	547
Ile	Asp	Glu	Lys	Ala	Tyr	His	Gly	Arg	Thr	Gly	Val	Cys	Leu	His	Thr	
				135					140					145		
tcc	tac	cac	cca	tcg	cgc	ttg	ctg	tgg	ctg	aaa	act	gag	ttc	gag	aaa	595
Ser	Tyr	His	Pro	Ser	Arg	Leu	Leu	Trp	Leu	Lys	Thr	Glu	Phe	Glu	Lys	
				150					155					160		
gag	ttc	aac	aaa	gcc	aag	tat	gtg	atg	acc	atc	ggt	gag	tac	gtc	tac	643
Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	Met	Thr	Ile	Gly	Glu	Tyr	Val	Tyr	
				170					175					180		
ttc	aaa	ctt	gca	ggc	atc	acc	gga	atg	gct	act	tcg	att	gcc	gcg	tgg	691
Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	Met	Ala	Thr	Ser	Ile	Ala	Ala	Trp	
				185					190					195		
agt	ggc	att	ttg	gac	gcc	cat	acc	ggc	gaa	ctt	gat	ctg	act	atc	ttg	739
Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	Gly	Glu	Leu	Asp	Leu	Thr	Ile	Leu	
				200					205					210		
gag	cac	atc	ggt	gtt	gat	ccg	gct	ctg	ttc	ggt	gag	atc	aga	aac	cct	787
Glu	His	Ile	Gly	Val	Asp	Pro	Ala	Leu	Phe	Gly	Glu	Ile	Arg	Asn	Pro	
				215					220					225		
gat	gaa	cca	gcc	acc	gat	gcc	aaa	gtt	gtc	gac	aaa	aag	tgg	aag	cac	835
Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	Val	Val	Asp	Lys	Lys	Trp	Lys	His	
				230					235					240		

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
250 255 260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
280 285 290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc	1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
295 300 305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa	1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
330 335 340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc	1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu	
375 380 385	
gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
390 395 400 405	
gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
410 415 420	
gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt	1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
440 445 450	
gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg	1507
Glu Gln Leu Glu Pro Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtggaaacg 1602
 Phe Asp Ala Leu Tyr Leu Lys Leu Val
 490

cgc 1605

<210> 320

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
 1 5 10 15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
 145 150 155 160

Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
 165 170 175

Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
 180 185 190

Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
 195 200 205

Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
 210 215 220

Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
 225 230 235 240

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
 245 250 255

Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr
260 265 270

Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro
275 280 285

Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser
290 295 300

Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala
305 310 315 320

Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu
325 330 335

Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe
340 345 350

Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr
355 360 365

Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly
370 375 380

Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met
385 390 395 400

Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val
405 410 415

Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp
 420 425 430

Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr
435 440 445

Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr
450 455 460

Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser
465 470 475 480

Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
485 490

<210> 321

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

$\langle 222 \rangle$ (101) .. (1111)

<223> ERXA01049

<400> 321

cacagtatgt ggagcagctg cgcgcgga aa tcgatgagaa ggcctaccac ggccgcaccg 60

gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115
Val Val Lys Thr Glu

														1			5		
ttc	gag	aaa	gag	ttc	aac	aaa	gcc	aag	tat	gtg	atg	acc	atc	ggt	gag	163			
Phe	Glu	Lys	Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	Met	Thr	Ile	Gly	Glu				
				10					15					20					
tac	gtc	tac	ttc	aaa	ctt	gca	ggc	atc	acc	gga	atg	gct	act	tcg	att	211			
Tyr	Val	Tyr	Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	Met	Ala	Thr	Ser	Ile				
				25					30					35					
gcc	gcg	tgg	agt	ggc	att	ttg	gac	gcc	cat	acc	ggc	gaa	ctt	gat	ctg	259			
Ala	Ala	Trp	Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	Gly	Glu	Leu	Asp	Leu				
				40					45					50					
act	atc	ttg	gag	cac	atc	ggt	gtt	gat	ccg	gct	ctg	ttc	ggt	gag	atc	307			
Thr	Ile	Leu	Glu	His	Ile	Gly	Val	Asp	Pro	Ala	Leu	Phe	Gly	Glu	Ile				
				55					60					65					
aga	aac	cct	gat	gaa	cca	gcc	acc	gat	gcc	aaa	gtt	gtc	gac	aaa	aag	355			
Arg	Asn	Pro	Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	Val	Val	Asp	Lys	Lys				
				70					75					80					
tgg	aag	cac	ctg	gaa	gaa	atc	cct	tgg	ttc	cat	gcc	att	cca	gac	ggc	403			
Trp	Lys	His	Leu	Glu	Glu	Ile	Pro	Trp	Phe	His	Ala	Ile	Pro	Asp	Gly				
				90					95					100					
tgg	cct	tcc	aac	att	ggc	cca	ggc	gcc	gtg	gat	tct	aaa	acc	gtc	gca	451			
Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp	Ser	Lys	Thr	Val	Ala				
				105					110					115					
gtc	gcc	gcc	gct	aca	tcc	ggc	gcc	atg	cgc	gtg	atc	ctt	ccg	agc	gtt	499			
Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro	Ser	Val				
				120					125					130					
ccc	gaa	cag	atc	ccc	tct	ggc	ctg	tgg	tgt	tac	cgc	gtt	tcc	cgc	gac	547			
Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser	Arg	Asp				
				135					140					145					
cag	tgc	atc	gtt	ggt	ggc	gca	ctc	aac	gac	gtc	gga	cgc	gcc	gtc	acc	595			
Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala	Val	Thr				
				150					155					160					
tgg	ctg	gaa	cgc	acc	att	atc	aag	cct	gaa	aac	ctc	gac	gaa	gtg	ctg	643			
Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu	Val	Leu				
				170					175					180					
atc	cgc	gaa	ccc	ctc	gaa	ggc	acc	cca	gct	gtc	ctg	ccg	ttc	ttc	tcc	691			
Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe	Phe	Ser				
				185					190					195					
ggg	gaa	cgc	tcc	atc	ggc	tgg	gca	gcc	tca	gcg	cag	gcc	acg	atc	acc	739			
Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr	Ile	Thr				
				200					205					210					
aac	att	cag	gaa	caa	acc	ggc	cct	gaa	cac	ttg	tgg	cgc	ggc	gtt	ttc	787			
Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly	Val	Phe				
				215					220					225					
gaa	gcc	ctc	gca	ctc	tcc	tac	cag	cgc	gtt	tgg	gaa	cac	atg	ggg	aaa	835			
Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met	Gly	Lys				
				230					235					240					

```

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883
Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
                250                255                260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931
Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
                265                270                275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc gcc acc gca ctt 979
Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
                280                285                290

atc gtc ctt gag cag ctc gaa cca ggc gcc acg cgc gcc acg cca cca 1027
Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
                295                300                305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075
Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
310                315                320                325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121
Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
                330                335

cagtggaacg cgc 1134

```

<210> 322

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 322

```

Val Val Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val
  1                5                10                15

Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly
                20                25                30

Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr
                35                40                45

Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
  50                55                60

Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
  65                70                75                80

Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
                85                90                95

Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
                100                105                110

Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val
                115                120                125

Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
  130                135                140

```

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
 145 150 155 160
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
 165 170 175
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
 180 185 190
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
 195 200 205
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
 210 215 220
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
 225 230 235 240
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
 245 250 255
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
 260 265 270
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
 275 280 285
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
 290 295 300
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
 305 310 315 320
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
 325 330 335

Val

<210> 323
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> FRXA01050

<400> 323
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60

aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro 5
 1

aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala 20
 10 15

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35

 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50

 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65

 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85

 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100

 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
 105 110 115

 tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
 120 125 130

 atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145

 tcc tac cac cca tcg cgc ttg ctg tgg tgaaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155

 gag 597

<210> 324

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
 1 5 10 15

 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

[illegible]

Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val	
120 125 130	
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct	547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala	
135 140 145	
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg	595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu	
150 155 160 165	
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt	643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe	
170 175 180	
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag	691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln	
185 190 195	
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg	739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu	
200 205 210	
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag	787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu	
215 220 225	
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat	835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp	
230 235 240 245	
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt	883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val	
250 255 260	
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg	931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu	
265 270 275	
gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac	979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp	
280 285 290	
gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac	1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn	
295 300 305	
gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt	1065
Val Ala Asp Phe Lys	
310	

<210> 326

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
1 5 10 15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30
 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 327

<211> 1077

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1054)

<223> RXN00872

<400> 327

gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcatc gtgagggtcg 60

ccacattcca	tcaaaaatga	gtgaagggtt	gcatcgccac	atg	act	aac	ttg	acg	115
				Met	Thr	Asn	Leu	Thr	
				1			5		

agc	act	cac	gaa	gtc	cta	gct	atc	ggc	cgc	ttg	ggc	gta	gat	att	tac	163
Ser	Thr	His	Glu	Val	Leu	Ala	Ile	Gly	Arg	Leu	Gly	Val	Asp	Ile	Tyr	
			10					15					20			

cca	ctt	caa	agt	gga	gta	gga	ctg	gcc	gat	ggt	caa	tct	ttc	ggc	aag	211
Pro	Leu	Gln	Ser	Gly	Val	Gly	Leu	Ala	Asp	Val	Gln	Ser	Phe	Gly	Lys	
			25				30						35			

tac	ctc	ggc	gga	agc	gca	gca	aac	gtt	tct	ggt	gca	gcc	gcc	cgc	cat	259
Tyr	Leu	Gly	Gly	Ser	Ala	Ala	Asn	Val	Ser	Val	Ala	Ala	Ala	Arg	His	
		40					45				50					

gga	cac	aat	tcc	gca	ctg	ctg	tcc	cgt	gtg	gga	aat	gat	cct	ttc	ggc	307
Gly	His	Asn	Ser	Ala	Leu	Leu	Ser	Arg	Val	Gly	Asn	Asp	Pro	Phe	Gly	
	55					60					65					

gag	tac	ctg	ctt	gct	gag	ctg	gag	cgt	ttg	ggc	gtg	gac	aac	cag	tac	355
Glu	Tyr	Leu	Leu	Ala	Glu	Leu	Glu	Arg	Leu	Gly	Val	Asp	Asn	Gln	Tyr	
	70				75				80					85		

ggt	gcc	acc	gat	cag	act	ttt	aag	acc	cca	gtg	acc	ttc	tgt	gaa	att	403
Val	Ala	Thr	Asp	Gln	Thr	Phe	Lys	Thr	Pro	Val	Thr	Phe	Cys	Glu	Ile	
				90				95						100		

ttc	cca	ccg	gat	gat	ttc	cca	ctg	tac	ttc	tac	cgc	gaa	cca	aag	gct	451
Phe	Pro	Pro	Asp	Asp	Phe	Pro	Leu	Tyr	Phe	Tyr	Arg	Glu	Pro	Lys	Ala	
			105				110					115				

ccg	gat	ctc	aat	att	gaa	tcc	gca	gac	gtc	agc	ctg	gac	gat	gtg	cgc	499
Pro	Asp	Leu	Asn	Ile	Glu	Ser	Ala	Asp	Val	Ser	Leu	Asp	Asp	Val	Arg	
		120					125					130				

gaa	gcc	gat	att	ttg	tgg	ttc	aca	ctc	act	ggt	ttc	agt	gaa	gag	cca	547
Glu	Ala	Asp	Ile	Leu	Trp	Phe	Thr	Leu	Thr	Gly	Phe	Ser	Glu	Glu	Pro	
	135					140					145					

agc	cgc	ggc	aca	cac	cgc	gag	atc	ttg	act	act	cgt	gcg	aac	cgt	cgc	595
Ser	Arg	Gly	Thr	His	Arg	Glu	Ile	Leu	Thr	Thr	Arg	Ala	Asn	Arg	Arg	
	150				155				160					165		

cac	acc	atc	ttt	gat	ctg	gac	tac	cga	cca	atg	ttc	tgg	gaa	tcc	cca	643
His	Thr	Ile	Phe	Asp	Leu	Asp	Tyr	Arg	Pro	Met	Phe	Trp	Glu	Ser	Pro	
			170					175						180		

gaa	gag	gcc	acc	aag	cag	gcg	gaa	tgg	gcg	ttg	cag	cat	tcc	acg	gtg	691
Glu	Glu	Ala	Thr	Lys	Gln	Ala	Glu	Trp	Ala	Leu	Gln	His	Ser	Thr	Val	
		185					190						195			